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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:00:44 ; Search time 31.4593 Seconds  
(without alignments)  
44.908 Million cell updates/sec

Title: US-09-753-139c-8

Perfect score: 34

Sequence: 1 CTCVP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	100.0	5	ABB83467	Abb83467 Tissue in
2	34	100.0	18	AAR65010	Aar65010 Tissue in
3	34	100.0	20	AAR31183	Aar31183 N-termina
4	34	100.0	36	ABB38484	Abb38484 Peptide #
5	34	100.0	36	AAM31928	Aam31928 Peptide #
6	34	100.0	36	ABB23640	Abb23640 Protein #
7	34	100.0	36	AAM71634	Aam71634 Human bon
8	34	100.0	36	AAM59099	Aam59099 Human bra
9	34	100.0	36	ABG53318	Abg53318 Human liv
10	34	100.0	36	ABG41448	Abg41448 Human pep
11	34	100.0	42	AAB25747	Aab25747 Human sec
12	34	100.0	47	AAP60276	Aap60276 N-termina
13	34	100.0	48	AAM48255	Aam48255 Bovine me
14	34	100.0	49	ABB82136	Abb82136 Bovine TI
15	34	100.0	49	ABB82135	Abb82135 Human tra
16	34	100.0	57	AAY70666	Aay70666 Human tra
17	34	100.0	83	AAM87683	Aam87683 Human imm
18	34	100.0	102	AAO02164	Aao02164 Human pol
19	34	100.0	115	AAW85462	Aaw85462 Secreted
20	34	100.0	115	ABP61805	Abp61805 Human pol
21	34	100.0	127	AAU99886	Aau99886 Human TIM
22	34	100.0	128	AAU99887	Aau99887 Human TIM
23	34	100.0	151	AAO07690	Aao07690 A rat int
24	34	100.0	151	AAO07594	Aao07594 A human i
25	34	100.0	151	ADB31994	Adb31994 Human par

26	34	100.0	160	3	AAY53891	Aay53891 Partial a
27	34	100.0	160	4	AAG66120	Aag66120 Human int
28	34	100.0	162	5	ABP42434	Abp42434 Human ova
29	34	100.0	173	3	AAY53893	Aay53893 Partial a
30	34	100.0	173	4	AAG66122	Aag66122 Human int
31	34	100.0	174	6	ABR58370	AbR58370 Human NOV
32	34	100.0	178	6	ABR58369	AbR58369 Human NOV
33	34	100.0	183	3	AAAB44149	AaB44149 Human can
34	34	100.0	183	3	AAY70658	Aay70658 Mature mu
35	34	100.0	183	6	AAE36024	Aae36024 Mouse int
36	34	100.0	184	2	AAE65000	Aae65000 Chicken i
37	34	100.0	184	5	AAU99875	Aau99875 Human tis
38	34	100.0	185	3	AAY70656	Aay70656 Mature hu
39	34	100.0	185	6	AAE36020	Aae36020 Human int
40	34	100.0	186	3	AAY70655	Aay70655 Mature hu
41	34	100.0	186	6	AAE36019	Aae36019 Human int
42	34	100.0	187	3	AAY70663	Aay70663 Mature hu
43	34	100.0	187	3	AAY70654	Aay70654 Mature hu
44	34	100.0	187	6	AAE36018	Aae36018 Human int
45	34	100.0	187	6	AAE36022	Aae36022 Human int

## ALIGNMENTS

## RESULT 1

ABB83467

ID ABB83467 standard; peptide; 5 AA.

XX ABB83467;

XX 30-SEP-2002 (first entry)

DT Tissue Inhibitor of Metalloproteinase, TIMP, derived peptide ChePep-6.

XX MMP; Matrix Metalloproteinase; zinc chelator; chronic wound; acute wound;

XX Tissue Inhibitor of Metalloproteinase; TIMP; connective tissue breakdown;

XX angiogenesis-associated disorder.

XX Synthetic.

XX WO200253173-A2.

XX 11-JUL-2002.

XX 21-DEC-2001; 2001WO-US049276.

XX 29-DEC-2000; 2000US-00753139.

XX (XIMB ) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Tyrrell DJ;

XX WPI; 2002-583595/62.

XX New matrix metalloproteinase regulator useful for the treatment of

XX chronic and acute wounds comprises a zinc chelator and a tissue inhibitor

XX of metalloproteinases-derived peptide.

XX Claim 6; Page 33; 57pp; English.

XX The present invention relates to Matrix Metalloproteinase (MMP)

XX regulators, which comprise a zinc chelator and a Tissue Inhibitor of

XX Metalloproteinases (TIMP)-derived peptide. The present sequence is one

XX such TIMP-derived peptide used to generate the MMP regulators. The MMP

XX regulators are useful for treating chronic and acute wounds, angiogenesis

XX -associated disorders; and other diseases and disorders involving

XX uncontrolled breakdown of connective tissues by MMPs. MMPs contain a zinc

XX molecule located in the active site, which participates in degrading

XX collagen. The binding specificity of the TIMP-derived peptide brings the

XX zinc chelator into molecular proximity of the MMP bound zinc in such a

XX way to allow ligation. This results in the regulation of the level of MMP

XX activity to promote wound healing by providing a MMP regulator having

CC high affinity and selectivity

XX Sequence 5 AA;

Query Match 100.0%; Score 34; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
 |||||  
 Db 1 CTCVP 5

# RESULT 2

AAR65010  
 ID AAR65010 standard; protein; 18 AA.

XX AC AAR65010;

XX DT 27-AUG-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 24-OCT-1995 (first entry)

XX DE Tissue inhibitor of metalloproteinase (TIMP-1) consensus.

XX KW Tissue inhibitor of metalloproteinase; diagnostic; therapeutic;  
 prophylaxis.

XX KW Mammalia.

XX OS Key

XX FH Location/Qualifiers

XX FT Inhibitory-site 2 /note= "Thr or Ser"

XX FT Misc-difference 4 /note= "Val or Ala"

XX FT Misc-difference 6 /note= "Pro or Thr"

XX FT Misc-difference 14 /note= "Asn or Ser"

XX FT Misc-difference 17 /note= "Ile or Val"

XX FT WO9505478-A1.

XX PN 23-FEB-1995.

XX PD 12-AUG-1994; 94WO-US009188.

XX PR 12-AUG-1993; 93US-00105263.

XX PR 13-DEC-1993; 93US-00167463.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Hawkes SP, Kishani NS, Yang T;

XX DR WPI; 1995-098775/13.

XX PT New human tissue inhibitor of metalloproteinase-3 - used to develop

XX PT prods. for diagnosis, therapy or prophylaxis of conditions with unwanted

XX PT matrix metalloproteinase activity.

XX PS Disclosure; Fig 10; 87pp; English.

XX CC The sequence represents a consensus sequence for the N-terminal of tissue

XX CC inhibitor of metalloproteinase-1 (TIMP-1) from human, mouse, rabbit,

XX CC cattle, pig and rat. In the figure, the sequence is compared with the

XX CC human, chicken and mouse TIMP-3 N-terminals, and with consensus sequence

XX CC of TIMP-2 (AAR65011). A probe based on the CHIMP-3 amino acid sequence

XX CC (AAR65000) is used to isolate DNA encoding human TIMP-3 from a human cDNA

XX CC library. Human TIMP-3 can be used for the diagnosis, therapy or

XX CC prophylaxis of conditions characterized by excess or unwanted matrix

XX CC metalloproteinase activity, e.g. neoplasias, tumor metastasis,

XX CC inflammatory disorders such as rheumatoid arthritis, ulcerations,

CC reaction to infection, periodontal disease or osteoporosis. It can also  
 CC be used in drug screening/design. (Updated on 25-MAR-2003 to correct PN  
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 34; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
 |||||  
 Db 1 CTCVP 5

# RESULT 3

AAR31183

ID AAR31183 standard; peptide; 20 AA.

XX AC AAR31183;

XX DT 25-MAR-2003 (revised)

XX DT 07-MAY-1993 (first entry)

XX DE N-terminal of monocyte specific chemotactic factor.

XX KW monocytes; leucocytes; white blood cells; neutrophils; chemotaxis;

XX KW inhibition; tissue metalloproteinase inhibitor; tissue healing;

XX KW wound repair; infection; infectious disease; neoplasia; tumour; cancer;

XX KW gelatinase.

XX OS Synthetic.

XX PN WO9222664-A1.

XX PD 23-DEC-1992.

XX PF 10-JUN-1992; 92WO-EP001298.

XX PR 13-JUN-1991; 91IT-MI001634.

XX PA (DOMP-) DOMPE SPA.

XX PI Mantovani A, Bottazzi B, Bertini R, Van Damme J;

XX DR WPI; 1993-018147/02.

XX PT Chemotactic factor specific for monocytes - obtd. from human ovarian

XX PT cancer cell line, and used for treating infection and neoplasias and for

XX PT promoting tissue and wound repair.

XX PS Claim 1; Fig 2; 18pp; English.

XX CC This sequence represents the N-terminal of a chemotactic factor. The

XX CC factor is able to induce migration of monocytes, but not neutrophils, and

XX CC has an apparent molecular weight of 25kD on SDS-PAGE. The factor inhibits

XX CC tissue metalloproteinases, such as gelatinase, and concomitantly induces

XX CC chemotactic migration of monocytes. It can be used to promote tissue

XX CC repair or wound healing and for the treatment of infectious disorders and

XX CC neoplasias. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-

XX CC MAR-2003 to correct PR field.)

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 34; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5

|||||

Db 1 CTCVP 5

[illegible]

```
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-488899/53.
XX XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 15; SEQ ID NO 25410; 530pp; English.
XX CC
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart (see
XX CC AB21535-AB41305). The present sequence is a protein encoded by one such
XX CC probe. The probes may be used for predicting, measuring and displaying
XX CC gene expression in samples derived from the human heart via microarrays.
XX CC By measuring gene expression, the probes are useful for predicting,
XX CC diagnosing, grading, staging, monitoring and prognosing diseases of the
XX CC human heart and vascular system e.g. cardiovascular disease,
XX CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 36 AA;

Query Match 100.0%; Score 34; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 26 CTCVP 30

RESULT 7
AAM71634
ID AAM71634 standard; protein; 36 AA.
XX AC AAM71634;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31940.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-488900/53.
XX XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
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XX PS Example 4; SEQ ID NO 31940; 658pp + Sequence Listing; English.
XX CC
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention
XX SQ Sequence 36 AA;

Query Match 100.0%; Score 34; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 26 CTCVP 30

RESULT 8
AAM59099
ID AAM59099 standard; protein; 36 AA.
XX AC AAM59099;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31204.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US0000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-483446/52.
XX XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO 31204; 650pp + Sequence Listing; English.
XX CC
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention
XX SQ Sequence 36 AA;

Query Match 100.0%; Score 34; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e+02;
```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
 Db 26 CTCVP 30

RESULT 9  
 ABG53318  
 ID ABG53318 standard; peptide; 36 AA.  
 XX AC ABG53318;  
 XX DT 25-FEB-2003 (first entry)  
 XX DE Human liver peptide, SEQ ID No 31966.  
 XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 XX KW hypercholesterolaemia; coronary heart disease.  
 XX OS Homo sapiens.  
 XX PN WO200157273-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US0000664.  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-00608408.  
 XX PR 03-AUG-2000; 2000US-00632366.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488898/53.  
 XX DR Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human adult liver.  
 XX PS Claim 27; SEQ ID NO 31966; 658pp; English.  
 XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (I) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
 CC liver single exon encoded peptides of the invention. Note: The sequence  
 CC information for this patent does not appear in the printed specification  
 CC but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 36 AA;  
 Query Match 100.0%; Score 34; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
 Db 26 CTCVP 30

RESULT 10  
 ABG41448  
 ID ABG41448 standard; peptide; 36 AA.  
 XX AC ABG41448;  
 XX DT 19-AUG-2002 (first entry)  
 XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 31113.  
 XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX OS Homo sapiens.  
 XX PN WO200186003-A2.  
 XX PD 15-NOV-2001.  
 XX PF 30-JAN-2001; 2001WO-US0000665.  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-00608408.  
 XX PR 03-AUG-2000; 2000US-00632366.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2002-114183/15.  
 XX DR Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX PS Claim 27; SEQ ID NO 31113; 634pp; English.  
 XX CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridise at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a peptide/protein encoded by a single exon probe of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pt\_sequences  
 CC  
 SQ Sequence 36 AA;

Query Match 100.0%; Score 34; DB 5; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCVP 5  
 |||||  
 Db 26 CTCVP 30

RESULT 11  
 ID AAB25747  
 AC AAB25747; protein; 42 AA.  
 XX  
 DT 04-DEC-2000 (first entry)  
 DE Human secreted protein sequence encoded by gene 23 SEQ ID NO:136.  
 KW Human; secreted protein; immunosuppressive; immunostimulant; nootropic;  
 KW antiinflammatory; cardiac; vulnery; antitumor; anticonvulsant;  
 KW antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic;  
 KW antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic;  
 KW gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator;  
 KW cancer; immune system disorder; hyperproliferative disorder; infection;  
 KW cardiovascular disorder; neurological disease; wound healing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200043495-A2.  
 XX  
 PD 27-JUL-2000.  
 XX  
 PF 18-JAN-2000; 2000WO-US000903.  
 XX  
 PR 19-JAN-1999; 99US-0116330P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Moore PA;  
 PI Komatsoulis G, Birse CE;  
 XX  
 DR WPI; 2000-499225/44.  
 XX  
 PT New isolated polynucleotide encoding a secreted protein useful for  
 PT preventing, treating or ameliorating a medical condition.  
 XX  
 PS Disclosure; Page 61; 45lpp; English.  
 XX  
 CC The polynucleotide sequences given in AAB25747 to AAB25755 encode the  
 CC human secreted proteins given in AAB25747 to AAB25755. Human secreted  
 CC proteins have activities based on the tissues and cells the genes are  
 CC expressed in. Examples of activities include: immunosuppressive;  
 CC immunostimulant; antiinflammatory; cardiac; vulnery; antitumor;  
 CC nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective;  
 CC antibacterial; antiparasitic; thrombolytic; anticoagulant;  
 CC antiarteriosclerotic and cytostatic. The secreted proteins and their  
 CC polynucleotides can be used in gene therapy and as vaccines, chemotaxis-

CC modulators and angiogenesis- modulators. The human secreted proteins and  
 CC polynucleotides can be used for diagnosing (the susceptibility to) a  
 CC pathological condition by determining the presence or absence of a  
 CC mutation in the polynucleotide or determining the presence or amount of  
 CC expression of the protein. The polynucleotides and proteins can also be  
 CC used in the treatment and diagnosis of cancer, diseases of the immune  
 CC system, hyperproliferative disorders, cardiovascular disorders and  
 CC neurological disease. They can also be used to promote wound healing and  
 CC to fight infection. AAB25747 to AAB25755 and AAB25664 represent sequences  
 CC used in the exemplification of the present invention  
 XX  
 SQ Sequence 42 AA;

Query Match 100.0%; Score 34; DB 3; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCVP 5  
 |||||  
 Db 30 CTCVP 34

RESULT 12  
 ID AAP60276  
 AC AAP60276; protein; 47 AA.  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 03-OCT-2002 (revised)  
 DT 08-AUG-1991 (first entry)  
 DE N-terminal sequence of fibroblast derived purified human natural  
 DE inhibitor of collagenases (NIC).  
 KW Metallo-proteinase inhibitor; wound healing; emphysema;  
 KW rheumatoid arthritis therapy; ulceration; tumour metastasis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN EP189784-A.  
 XX  
 PD 06-AUG-1986.  
 XX  
 PF 16-JAN-1986; 86EP-00100482.  
 XX  
 PR 18-JAN-1985; 85US-00692808.  
 XX  
 PA (SEAR ) SEARLE & CO G D.  
 XX  
 PI Galloway WA, Clissold PM, McCullagh KG;  
 XX  
 DR WPI; 1986-205910/32.  
 XX  
 PT New human natural inhibitor of collagenase - for treating e.g. rheumatoid  
 PT arthritis or ulceration, and new DNA sequences coding for it.  
 XX  
 PS Example; Fig 5; 5lpp; English.  
 XX  
 CC The patentors claim the AA SQ of human NIC, DNA sequences coding for NIC,  
 CC and its RNA analogues and plasmids contg. this DNA. NIC inhibits the  
 CC activity of metallo-proteinases, esp. of collagenase, proteoglycanase,  
 CC gelatinase or a leucocyte, macrophage or tumour cell metallo-proteinase.  
 CC (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003  
 CC to correct PA field.)  
 XX  
 SQ Sequence 47 AA;  
 Query Match 100.0%; Score 34; DB 1; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CTCVP 5
Db      1 CTCVP 5

RESULT 13
AAW48255
ID      AAW48255 standard; protein; 48 AA.
XX      AC
XX      AAW48255;
XX      16-JUL-1998 (first entry)
XX      DE
XX      Bovine metalloproteinase inhibitor protein fragment (peak 2).
XX      KW
XX      Metalloproteinase inhibitor; extracellular connective tissue matrix;
XX      treatment; degradative disease; dystrophic epidermolysis bullosa;
XX      rheumatoid arthritis; ulceration; peridontal disease; emphysema;
XX      bone disease; tumour metastasis; invasion; bovine.
XX      OS
XX      Bos taurus.
XX      PN
XX      US5714465-A.
XX      PD
XX      03-FEB-1998.
XX      PF
XX      11-MAR-1994; 94US-00212660.
XX      PR
XX      19-MAY-1989; 89US-00355027.
XX      29-MAR-1990; 90US-00501904.
XX      03-JUN-1991; 91US-00710728.
XX      06-JUL-1993; 93US-00087021.
XX      PA
XX      (AMGE-) AMGEN INC.
XX      PI
XX      Langley KE, Boone TC, Declerck YA;
XX      WPI; 1998-158348/14.
XX      PT
XX      Inhibition of tumour cell dissemination - by administering human metallo-
XX      proteinase inhibitor polypeptide.
XX      PS
XX      Example 2; Col 17-18; 60pp; English.
XX      CC
XX      This sequence represents a fragment of bovine metalloproteinase inhibitor
XX      (described as peak 2) which can be used for tumour cell dissemination or
XX      to inhibit tumour metastasis in a mammal. Metalloproteinases degrade
XX      extracellular connective tissue matrix and inhibitors of
XX      metalloproteinases can be used in the treatment of degradative diseases
XX      of connective tissue, e.g., dystrophic epidermolysis bullosa, rheumatoid
XX      arthritis, corneal, epidermal or gastric ulceration, peridontal disease,
XX      emphysema, bone disease and tumour metastasis or invasion
XX      SQ
XX      Sequence 48 AA;

Query Match      100.0%; Score 34; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      1 CTCVP 5

RESULT 14
ABB82136
ID      ABB82136 standard; protein; 49 AA.
XX      AC
XX      ABB82136;
XX      05-DEC-2002 (first entry)
XX      DT
XX      05-DEC-2002 (first entry)
XX      DE
XX      Bovine TIMP protein fragment.

QY      1 CTCVP 5
Db      1 CTCVP 5

RESULT 15
ABB82135
ID      ABB82135 standard; protein; 49 AA.
XX      AC
XX      ABB82135;
XX      05-DEC-2002 (first entry)
XX      DT
XX      Human TIMP protein fragment.
XX      DE
XX      Human TIMP protein fragment.

XX      Metalloproteinase inhibitor; cytostatic; antirheumatic; antiarthritic;
XX      antianemic; neuroprotective; osteopathic; dermatological; vulnery;
XX      gene therapy; angiogenesis; transgenic; bovine; TIMP.
XX      OS
XX      Bos sp.
XX      PN
XX      US2002090654-A1.
XX      PD
XX      11-JUL-2002.
XX      PF
XX      21-FEB-1997; 97US-00803954.
XX      PR
XX      19-MAY-1989; 89US-00355027.
XX      29-MAR-1990; 90US-00501904.
XX      03-JUN-1991; 91US-00710728.
XX      06-JUL-1993; 93US-00087021.
XX      11-MAR-1994; 94US-00212660.
XX      PA
XX      (LANG/) LANGLEY K E.
XX      PA
XX      (DECL/) DECLERCK Y A.
XX      PA
XX      (BOON/) BOONE T C.
XX      PI
XX      Langley KE, Declerck YA, Boone TC;
XX      WPI; 2002-681724/73.
XX      CC
XX      Novel purified and isolated metalloproteinase inhibitor polypeptide
XX      useful for inhibiting tumor cell dissemination, for treating rheumatoid
XX      arthritis, Paget's disease, osteoporosis, anemia and immunological
XX      disorders.
XX      PS
XX      Example 2; Page 10; 65pp; English.
XX      CC
XX      The invention relates to a metalloproteinase inhibitor (MI) polypeptide.
XX      The MI polypeptide is useful for inhibiting tumour cell dissemination or
XX      for treating rheumatoid arthritis in a mammal. It is useful for treating
XX      connective tissue disorders characterized by matrix degradation, for
XX      treating disorders where excessive matrix losses are caused by
XX      metalloproteinase activity, for promoting wound healing following surgery
XX      or other wound situations, for treating dystrophic epidermolysis bullosa,
XX      anemia, immunological disorders such as autoimmune disease (e.g. multiple
XX      arthritis), for preventing or retarding tumour development, emphysema,
XX      Paget's disease of bone, osteoporosis, scleroderma, pressure atrophy of
XX      bone or tissues as in bedsores, cholesteatoma, and abnormal wound
XX      healing. The DNA sequences are useful for effecting the large scale
XX      synthesis of the polypeptide and in developing transgenic mammalian
XX      species which may serve as eukaryotic hosts for production of MI and MI
XX      products, and for identifying human MI gene disorders at the DNA level.
XX      The present sequence represents a bovine TIMP (tissue inhibitor of
XX      metalloproteinases) protein fragment
XX      SQ
XX      Sequence 49 AA;

Query Match      100.0%; Score 34; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      1 CTCVP 5

```

KW Metalloproteinase inhibitor; cytostatic; antirheumatic; antiarthritic;  
 KW antianemic; neutroprotective; osteopathic; dermatological; vulnerary;  
 KW gene therapy; angiogenesis; transgenic; human; TIMP.

XX Homo sapiens.

XX US2002090654-A1.

XX 11-JUL-2002.

XX 21-FEB-1997; 97US-00803954.

XX 19-MAY-1989; 89US-00355027.

XX 29-MAR-1990; 90US-00501904.

XX 03-JUN-1991; 91US-00710728.

XX 06-JUL-1993; 93US-00087021.

XX 11-MAR-1994; 94US-00212660.

XX (LANG/) LANGLEY K E.

XX (DECL/) DECLERCK Y A.

XX (BOON/) BOONE T C.

XX Langley KE, Declerck YA, Boone TC;

XX WPI; 2002-681724/73.

XX Novel purified and isolated metalloproteinase inhibitor polypeptide

XX useful for inhibiting tumor cell dissemination, for treating rheumatoid

XX arthritis, Paget's disease, osteoporosis, anemia and immunological

XX disorders.  
 XX Example 2; Page 10; 65pp; English.

XX The invention relates to a metalloproteinase inhibitor (MI) polypeptide.  
 XX The MI polypeptide is useful for inhibiting tumour cell dissemination or  
 XX for treating rheumatoid arthritis in a mammal. It is useful for treating  
 XX connective tissue disorders characterized by matrix degradation, for  
 XX treating disorders where excessive matrix losses are caused by  
 XX metalloproteinase activity, for promoting wound healing following surgery  
 XX or other wound situations, for treating dystrophic epidermolysis bullosa,  
 XX anemia, immunological disorders such as autoimmune disease (e.g. multiple  
 XX arthritis), for preventing or retarding tumour development, emphysema,  
 XX Paget's disease of bone, osteoporosis, scleroderma, pressure atrophy of  
 XX bone or tissues as in bedsores, cholesteatoma, and abnormal wound  
 XX healing. The DNA sequences are useful for effecting the large scale  
 XX synthesis of the polypeptide and in developing transgenic mammalian  
 XX species which may serve as eukaryotic hosts for production of MI and MI  
 XX products, and for identifying human MI gene disorders at the DNA level.  
 XX The present sequence represents a human TIMP (tissue inhibitor of  
 XX metalloproteinases) protein fragment

XX Sequence 49 AA;

XX Query Match 100.0%; Score 34; DB 5; Length 49;  
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
 |||||

Db 1 CTCVP 5

Search completed: April 8, 2004, 11:10:04  
 Job time : 33.5583 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:02:14 ; Search time 9.09722 Seconds  
(without alignments)  
28.375 Million cell updates/sec

Title: US-09-753-139C-8

Perfect score: 34

Sequence: 1 CTCVP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/2/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/prodata/2/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/prodata/2/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/prodata/2/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/prodata/2/iaa/PCTUS COMB.pcp.\*
- 6: /cgn2\_6/prodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	15	1	US-08-179-481-32
2	34	100.0	106	4	US-09-452-817-2
3	34	100.0	151	4	US-09-480-297A-6
4	34	100.0	160	4	US-09-231-788-12
5	34	100.0	184	4	US-09-452-817-1
6	34	100.0	202	4	US-09-480-297A-8
7	34	100.0	202	4	US-09-747-259-8
8	34	100.0	202	4	US-09-816-744-8
9	34	100.0	205	4	US-09-724-864-37
10	34	100.0	205	4	US-09-480-297A-12
11	34	100.0	206	4	US-08-134-231C-24
12	34	100.0	206	4	US-08-728-160-24
13	34	100.0	207	1	US-08-588-163-5
14	34	100.0	207	2	US-09-111-070-5
15	34	100.0	207	4	US-08-849-764C-5
16	34	100.0	207	4	US-09-862-087-5
17	34	100.0	207	4	US-08-463-261B-11
18	34	100.0	207	4	US-09-540-530-1
19	34	100.0	207	4	US-08-134-231C-22
20	34	100.0	207	4	US-08-134-231C-23
21	34	100.0	207	4	US-08-728-160-22
22	34	100.0	207	4	US-08-728-160-23
23	34	100.0	212	4	US-08-134-231C-29
24	34	100.0	212	4	US-08-728-160-29
25	34	100.0	1079	3	US-09-136-652-2
26	34	100.0	2409	6	5180808-2
27	33	97.1	20	4	US-08-464-496-1

Sequence 1, Appli  
Patent No. 5196194  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 6, Appli  
Sequence 7, Appli  
Sequence 8, Appli  
Sequence 9, Appli  
Sequence 10, Appli  
Sequence 11, Appli  
Sequence 12, Appli  
Sequence 13, Appli  
Sequence 14, Appli  
Sequence 15, Appli  
Sequence 16, Appli  
Sequence 17, Appli

#### ALIGNMENTS

RESULT 1  
US-08-179-481-32  
; Sequence 32, Application US/08179481  
; Patent No. 5624816  
; GENERAL INFORMATION:  
; APPLICANT: CARRAWAY, KERMIT L.  
; APPLICANT: CARROTHERS, CARRAWAY, CORALIE A.  
; APPLICANT: FREGIEN, NEVIS L.  
; TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND  
; NUMBER OF SEQUENCES: 125  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/179,481  
; FILING DATE: 28-DEC-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,521  
; FILING DATE: 30-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-179-481-32

Query Match 100.0%; Score 34; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CTCVP 5
Db 9 CTCVP 13

RESULT 2
US-09-452-817-2
; Sequence 2, Application US/09452817
; Patent No. 6342374
; GENERAL INFORMATION:
; APPLICANT: Carmichael, David F
; APPLICANT: Anderson, David C
; APPLICANT: Stricklin, George P
; APPLICANT: Welgus, Howard G
; TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System
; TITLE OF INVENTION: For Using Same And Recombinant-DNA Method For
; FILE REFERENCE: Serial No. 6342374 09/452,817
; CURRENT APPLICATION NUMBER: US/09/452,817
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 08/474,553
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/050,739
; PRIOR FILING DATE: 1993-04-21
; PRIOR APPLICATION NUMBER: 07/853,018
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: 07/517,475
; PRIOR FILING DATE: 1990-05-01
; PRIOR APPLICATION NUMBER: 07/320,923
; PRIOR FILING DATE: 1989-03-08
; PRIOR APPLICATION NUMBER: 06/784,319
; PRIOR FILING DATE: 1985-10-04
; PRIOR APPLICATION NUMBER: 06/699,181
; PRIOR FILING DATE: 1985-02-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-452-817-2

Query Match 100.0%; Score 34; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 1 CTCVP 5

RESULT 3
US-09-480-297A-6
; Sequence 6, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-297A-6

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Query Match 100.0%; Score 34; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 137 CTCVP 141

RESULT 4
US-09-231-788-12
; Sequence 12, Application US/09231788A
; Patent No. 6486301
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Interleukin-20
; FILE REFERENCE: PF399P1
; CURRENT APPLICATION NUMBER: US/09/231,788A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: 60/052,870
; EARLIER FILING DATE: 1997-07-16
; EARLIER APPLICATION NUMBER: 60/055,952
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/060,140
; EARLIER FILING DATE: 1997-09-26
; EARLIER APPLICATION NUMBER: 09/115,832
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-231-788-12

Query Match 100.0%; Score 34; DB 4; Length 160;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 125 CTCVP 129

RESULT 5
US-09-452-817-1
; Sequence 1, Application US/09452817
; Patent No. 6342374
; GENERAL INFORMATION:
; APPLICANT: Carmichael, David F
; APPLICANT: Anderson, David C
; APPLICANT: Stricklin, George P
; APPLICANT: Welgus, Howard G
; TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System
; TITLE OF INVENTION: For Using Same And Recombinant-DNA Method For
; FILE REFERENCE: Serial No. 6342374 09/452,817
; CURRENT APPLICATION NUMBER: US/09/452,817
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 08/474,553
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/050,739
; PRIOR FILING DATE: 1993-04-21
; PRIOR APPLICATION NUMBER: 07/853,018
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: 07/517,475
; PRIOR FILING DATE: 1990-05-01
; PRIOR APPLICATION NUMBER: 07/320,923
; PRIOR FILING DATE: 1989-03-08
; PRIOR APPLICATION NUMBER: 06/784,319
; PRIOR FILING DATE: 1985-10-04
; PRIOR APPLICATION NUMBER: 06/699,181
; PRIOR FILING DATE: 1985-02-05

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; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-452-817-1

Query Match 100.0%; Score 34; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
|||  
Db 1 CTCVP 5

## RESULT 6

US-09-480-297A-8  
; Sequence 8, Application US/09480297A  
; Patent No. 6562578  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS  
; FILE REFERENCE: DK0917K  
; CURRENT APPLICATION NUMBER: US/09/480,297A  
; CURRENT FILING DATE: 2000-01-10  
; PRIOR APPLICATION NUMBER: 60/115,506  
; PRIOR FILING DATE: 1999-01-11  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 202  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-480-297A-8

Query Match 100.0%; Score 34; DB 4; Length 202;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
|||  
Db 167 CTCVP 171

## RESULT 7

US-09-747-259-8  
; Sequence 8, Application US/09747259  
; Patent No. 6569645  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Tumas, Daniel  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William  
; APPLICANT: Yansura, Daniel  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
; FILE REFERENCE: P1381R1C1P1(US)  
; CURRENT APPLICATION NUMBER: US/09/747,259

; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 09/311,832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US 60/172,096  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: PCT/US99/31274  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: US 60/175,481  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: PCT/US00/04341  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 60/191,007  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: PCT/US00/07532  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/213,087  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: US 09/644,848  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/242,837  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: PCT/US00/30873  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: US 60/253,646  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 39  
; SEQ ID NO 8  
; LENGTH: 202  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-747-259-8

Query Match 100.0%; Score 34; DB 4; Length 202;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
|||  
Db 167 CTCVP 171

## RESULT 8

US-09-816-744-8  
; Sequence 8, Application US/09816744  
; Patent No. 6579520  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Tumas, Daniel  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William  
; APPLICANT: Yansura, Daniel  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
; FILE REFERENCE: P1381R1C1P2(US)  
; CURRENT APPLICATION NUMBER: US/09/816,744

; CURRENT FILING DATE: 2001-03-22  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 39  
; SEQ ID NO 8  
; LENGTH: 202  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-816-744-8

Query Match 100.0%; Score 34; DB 4; Length 202;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
Db 167 CTCVP 171

RESULT 9  
US-09-724-864-37  
; Sequence 37, Application US/09724864  
; Patent No. 6380362  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; FILE REFERENCE: 11000.105001  
; CURRENT APPLICATION NUMBER: US/09/724,864  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-724-864-37

Query Match 100.0%; Score 34; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
Db 174 CTCVP 178

RESULT 10  
US-09-480-297A-12  
; Sequence 12, Application US/09480297A  
; Patent No. 6562578  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Bazan, J. Fernando  
; APPLICANT: Kastelein, Robert A.  
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS  
; FILE REFERENCE: DX0917K  
; CURRENT APPLICATION NUMBER: US/09/480,297A  
; CURRENT FILING DATE: 2000-01-10  
; PRIOR APPLICATION NUMBER: 60/115,506  
; PRIOR FILING DATE: 1999-01-11  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-480-297A-12

Query Match 100.0%; Score 34; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTCVP 5  
Db 174 CTCVP 178

RESULT 11  
US-08-134-231C-24  
; Sequence 24, Application US/08134231C  
; Patent No. 6562596  
; GENERAL INFORMATION:  
; APPLICANT: Silbiger, Scott M.  
; TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type  
; Three (TIMP-3) Composition and Methods  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: District of Columbia  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/134,231C  
; FILING DATE: 06-Oct-1993  
; CLASSIFICATION: <Unknown>  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 206 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-08-134-231C-24

Query Match 100.0%; Score 34; DB 4; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
Db 24 CTCVP 28

RESULT 12  
US-08-728-160-24  
; Sequence 24, Application US/08728160  
; Patent No. 6683155  
; GENERAL INFORMATION:  
; APPLICANT: Silbiger, Scott M.  
; TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type  
; Three (TIMP-3) Composition and Methods  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc./Patent Operations/KMP  
; STREET: 1640 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: US/08/728,160  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/134,231  
;; FILING DATE:  
;; INFORMATION FOR SEQ ID NO: 24:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 206 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-728-160-24

Query Match 100.0%; Score 34; DB 4; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
Db 24 CTCVP 28

RESULT 13  
US-08-588-163-5  
; Sequence 5, Application US/08588163  
; Patent No. 5643752  
; GENERAL INFORMATION:  
; APPLICANT: Hawking, Phillip R.  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/588,163  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 207 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: METALLOPROTEINASES  
; CLONE: TIMP-1

US-08-588-163-5

Query Match 100.0%; Score 34; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
Db 24 CTCVP 28

RESULT 14  
US-09-111-070-5  
; Sequence 5, Application US/09111070  
; Patent No. 5914392  
; GENERAL INFORMATION:  
; APPLICANT: Hawking, Phillip R.  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/111,070  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/588,163  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 207 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: METALLOPROTEINASES  
; CLONE: TIMP-1  
; US-09-111-070-5

Query Match 100.0%; Score 34; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
Db 24 CTCVP 28

RESULT 15  
US-08-849-764C-5  
; Sequence 5, Application US/08849764C  
; Patent No. 6300310

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; GENERAL INFORMATION:
; APPLICANT: GREENE, JOHN M
; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
; METALLOPROTEINASE-4
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,764C
; FILING DATE: 19-Sep-1997
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PFI48US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-849-764C-5

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Query Match          100.0%; Score 34; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CTCVP 5
Db 24 CTCVP 28

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Search completed: April 8, 2004, 11:20:31
Job time : 10.0972 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:16:30 ; Search time 21.6667 Seconds  
(without alignments)  
60.678 Million cell updates/sec

Title: US-09-753-139C-8

Perfect score: 34

Sequence: 1 CTCVP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	5	10	US-09-753-139C-8
2	34	100.0	36	9	US-09-864-761-38938
3	34	100.0	54	12	US-10-424-599-213246
4	34	100.0	61	12	US-10-424-599-279533
5	34	100.0	87	12	US-10-424-599-236048
6	34	100.0	115	9	US-09-745-763-46
7	34	100.0	127	14	US-10-025-514-22
8	34	100.0	128	14	US-10-025-514-24
9	34	100.0	151	14	US-10-366-791-6
10	34	100.0	153	12	US-10-425-114-40481
11	34	100.0	160	9	US-09-731-816-4
12	34	100.0	160	10	US-09-320-713-4
13	34	100.0	160	14	US-10-153-770-4
14	34	100.0	160	14	US-10-277-726A-12
15	34	100.0	160	14	US-10-397-282-4

16	34	100.0	162	15	US-10-264-049-3566	Sequence 3566, Ap
17	34	100.0	173	9	US-09-731-816-32	Sequence 32, Appl
18	34	100.0	173	10	US-09-320-713-32	Sequence 32, Appl
19	34	100.0	173	14	US-10-153-770-32	Sequence 32, Appl
20	34	100.0	173	14	US-10-397-282-32	Sequence 32, Appl
21	34	100.0	174	12	US-10-262-839-16	Sequence 16, Appl
22	34	100.0	178	12	US-10-262-839-14	Sequence 14, Appl
23	34	100.0	183	9	US-09-925-301-1594	Sequence 1594, Ap
24	34	100.0	184	14	US-10-025-514-6	Sequence 6, Appl
25	34	100.0	199	12	US-10-210-172-6	Sequence 6, Appl
26	34	100.0	199	12	US-10-210-172-8	Sequence 8, Appl
27	34	100.0	202	9	US-09-874-503-8	Sequence 8, Appl
28	34	100.0	202	10	US-09-816-744-8	Sequence 8, Appl
29	34	100.0	202	10	US-09-747-259-8	Sequence 8, Appl
30	34	100.0	202	10	US-09-908-827-8	Sequence 8, Appl
31	34	100.0	202	12	US-10-219-535-88	Sequence 88, Appl
32	34	100.0	202	12	US-10-232-230-88	Sequence 88, Appl
33	34	100.0	202	12	US-10-408-385-8	Sequence 88, Appl
34	34	100.0	202	13	US-10-000-157-8	Sequence 8, Appl
35	34	100.0	202	14	US-10-227-884-88	Sequence 88, Appl
36	34	100.0	202	14	US-10-230-163-88	Sequence 88, Appl
37	34	100.0	202	14	US-10-230-338-88	Sequence 88, Appl
38	34	100.0	202	14	US-10-218-631-88	Sequence 88, Appl
39	34	100.0	202	14	US-10-230-414-88	Sequence 88, Appl
40	34	100.0	202	14	US-10-216-159A-88	Sequence 88, Appl
41	34	100.0	202	14	US-10-218-849-88	Sequence 88, Appl
42	34	100.0	202	14	US-10-227-873-88	Sequence 88, Appl
43	34	100.0	202	14	US-10-227-883-88	Sequence 88, Appl
44	34	100.0	202	14	US-10-219-076-88	Sequence 88, Appl
45	34	100.0	202	14	US-10-230-434-88	Sequence 88, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-753-139C-8  
; Sequence 8, Application US/09753139C  
; Publication No. US20030073808A1

; GENERAL INFORMATION:

; APPLICANT: Quirk, Stephen

; APPLICANT: Tyrrell, David

; TITLE OF INVENTION: Design and Use of Advanced Zinc Chelating Peptides to Regulate Ma

; TITLE OF INVENTION: Metalloproteases

; FILE REFERENCE: 44039-227522 11301-0200

; CURRENT APPLICATION NUMBER: US/09/753,139C

; CURRENT FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 8

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-09-753-139C-8

Query Match 100.0%; Score 34; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 1 CTCVP 5

#### RESULT 2

US-09-864-761-38938  
; Sequence 38938, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.





;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

;; FILE REFERENCE: 38-21(53223)B  
;; CURRENT APPLICATION NUMBER: US/10/424,599

;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 285684

;; SEQ ID NO 236048

;; LENGTH: 87

;; TYPE: PRT

;; ORGANISM: Glycine max

;; FEATURE:

;; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_5517C.1.pcp  
US-10-424-599-236048

Query Match 100.0%; Score 34; DB 12; Length 87;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 28 CTCVP 32

RESULT 6

US-09-745-763-46

;; Sequence 46, Application US/09745763

;; Patent No. US20020065394A1

;; GENERAL INFORMATION:

;; APPLICANT: Jacobs, Kenneth

;; McCoy, John M.

;; LaVallie, Edward R.

;; Collins-Racie, Lisa A.

;; Evans, Cheryl

;; Merberg, David

;; Treacy, Maurice

;; Spaulding, Vikki

;; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

;; NUMBER OF SEQUENCES: 219

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Genetics Institute, Inc.

;; STREET: 87 CambridgePark Drive

;; CITY: Cambridge

;; STATE: MA

;; COUNTRY: U.S.A.

;; ZIP: 02140

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patentin Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/745,763

;; FILING DATE: 18-Jun-2000

;; CLASSIFICATION: <Unknown>

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Sprunger, Suzanne A.

;; REGISTRATION NUMBER: 41,323

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617) 498-8284

;; TELEFAX: (617) 876-5851

;; INFORMATION FOR SEQ ID NO: 46:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 115 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: <unknown>

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-09-745-763-46

Query Match

Best Local Similarity 100.0%; Score 34; DB 9; Length 115;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 48 CTCVP 52

RESULT 7

US-10-025-514-22

;; Sequence 22, Application US/10025514

;; Publication No. US20030073217A1

;; GENERAL INFORMATION:

;; APPLICANT: Philip J. BARR

;; Applicant: Helen GIBSON

;; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND

;; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE

;; FILE REFERENCE: 368292000200

;; CURRENT APPLICATION NUMBER: US/10/025,514

;; CURRENT FILING DATE: 2002-04-03

;; PRIOR APPLICATION NUMBER: U.S. 60/256,699

;; PRIOR FILING DATE: 2000-12-18

;; PRIOR APPLICATION NUMBER: U.S. 60/331,966

;; PRIOR FILING DATE: 2001-11-20

;; NUMBER OF SEQ ID NOS: 33

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 22

;; LENGTH: 127

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-025-514-22

Query Match

Best Local Similarity 100.0%; Score 34; DB 14; Length 127;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 2 CTCVP 6

RESULT 8

US-10-025-514-24

;; Sequence 24, Application US/10025514

;; Publication No. US20030073217A1

;; GENERAL INFORMATION:

;; APPLICANT: Philip J. BARR

;; Applicant: Helen GIBSON

;; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND

;; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE

;; FILE REFERENCE: 368292000200

;; CURRENT APPLICATION NUMBER: US/10/025,514

;; CURRENT FILING DATE: 2002-04-03

;; PRIOR APPLICATION NUMBER: U.S. 60/256,699

;; PRIOR FILING DATE: 2000-12-18

;; PRIOR APPLICATION NUMBER: U.S. 60/331,966

;; PRIOR FILING DATE: 2001-11-20

;; NUMBER OF SEQ ID NOS: 33

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 24

;; LENGTH: 128

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-025-514-24

Query Match

Best Local Similarity 100.0%; Score 34; DB 14; Length 128;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 2 CTCVP 6

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RESULT 9
US-10-366-791-6
; Sequence 6, Application US/10366791
; Publication No. US20030170827A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/10/366,791
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US/09/480,297A
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-791-6

Query Match      100.0%; Score 34; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      137 CTCVP 141

RESULT 10
US-10-425-114-40481
; Sequence 40481, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40481
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-013-H8_FLI pep
US-10-425-114-40481

Query Match      100.0%; Score 34; DB 12; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      143 CTCVP 147

RESULT 11
US-09-731-816-4
; Sequence 4, Application US/09731816
; Patent No. US20010023070A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Interleukins-21 and 22
; FILE REFERENCE: PF470P1
; CURRENT APPLICATION NUMBER: US/09/731,816
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,837
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-731-816-4

Query Match      100.0%; Score 34; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      125 CTCVP 129

RESULT 12
US-09-320-713-4
; Sequence 4, Application US/09320713
; Publication No. US20030003545A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard Ebner
; APPLICANT: Steven M. Ruben
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470
; CURRENT APPLICATION NUMBER: US/09/320,713
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/087,340
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-320-713-4

Query Match      100.0%; Score 34; DB 10; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      125 CTCVP 129

RESULT 13
US-10-153-770-4
; Sequence 4, Application US/10153770

```

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; Publication No. US20030092133A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard Ebner
; APPLICANT: Steven M. Ruben
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470
; CURRENT APPLICATION NUMBER: US/10/153,770
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-770-4

```

```

Query Match      100.0%; Score 34; DB 14; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 CTCVP 5
Db      125 CTCVP 129

```

## RESULT 14

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US-10-277-726A-12
; Sequence 12, Application US/10277726A
; Publication No. US20030180892A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Interleukin-20
; FILE REFERENCE: PF399P1D1
; CURRENT APPLICATION NUMBER: US/10/277,726A
; CURRENT FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 09/231,788
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 09/115,832
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/060,140
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 60/055,952
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/052,870
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-277-726A-12

```

```

Query Match      100.0%; Score 34; DB 14; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CTCVP 5
Db      125 CTCVP 129

```

## RESULT 15

```

US-10-397-282-4
; Sequence 4, Application US/10397282

```

```

; Publication No. US20030186387A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Interleukins-21 and 22
; FILE REFERENCE: PF470P1
; CURRENT APPLICATION NUMBER: US/10/397,282
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US/09/731,816
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,837
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-397-282-4

```

```

Query Match      100.0%; Score 34; DB 14; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CTCVP 5
Db      125 CTCVP 129

```

```

Search completed: April 8, 2004, 11:55:44
Job time : 21.6667 secs

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*This Page Blank (uspto)*

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

QM protein - protein search, using sw model

Run on: April 8, 2004, 11:00:44 ; Search time 20.5556 Seconds  
(without alignments)  
76.748 Million cell updates/sec

Title: US-09-753-139C-8

Perfect score: 34

Sequence: 1 CTCVP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	44	5	Q7YVW4
2	34	100.0	44	5	Q7YVU3
3	34	100.0	84	10	Q9LRE1
4	34	100.0	106	5	Q81632
5	34	100.0	121	12	Q80NT4
6	34	100.0	169	4	Q96QM2
7	34	100.0	196	11	Q8K599
8	34	100.0	202	4	Q8TAD2
9	34	100.0	205	11	Q8K4C4
10	34	100.0	292	4	Q96RY6
11	34	100.0	400	5	Q9GRG2
12	34	100.0	487	5	Q8MSX5
13	34	100.0	579	12	Q98201
14	34	100.0	608	11	Q8OV54
15	34	100.0	646	4	Q8NEJ2
16	34	100.0	668	5	Q9VAU4

17	34	100.0	670	4	Q9Y6R3	Q9Y6r3 homo sapien
18	34	100.0	673	4	Q86WK8	Q86wk8 homo sapien
19	34	100.0	721	5	Q95YG0	Q95yg0 ciona savig
20	34	100.0	732	6	Q95L62	Q95l62 sus scrofa
21	34	100.0	739	12	Q9YQY1	Q9yqy1 ranid herpe
22	34	100.0	955	4	Q96DN2	Q96dn2 homo sapien
23	34	100.0	995	4	Q9NRZ1	Q9nrz1 homo sapien
24	34	100.0	1035	4	O15153	O15153 homo sapien
25	34	100.0	1079	4	Q9Y6R1	Q9y6r1 homo sapien
26	34	100.0	1079	4	Q9UIC0	Q9uic0 homo sapien
27	34	100.0	1079	4	Q9UIC1	Q9uic1 homo sapien
28	34	100.0	1079	4	Q9H262	Q9h262 homo sapien
29	34	100.0	1079	4	Q9UP50	Q9up50 homo sapien
30	34	100.0	1079	11	Q9QYA6	Q9qya6 rattus norv
31	34	100.0	2146	5	Q9VC97	Q9vc97 drosophila
32	34	100.0	7154	5	Q81FD8	Q81fd8 trypanosoma
33	33	97.1	41	12	Q9E2T0	Q9e2t0 hepatitis b
34	33	97.1	41	12	Q9E2S4	Q9e2s4 hepatitis b
35	33	97.1	41	12	Q9E2S8	Q9e2s8 hepatitis b
36	33	97.1	41	12	Q9E2T1	Q9e2t1 hepatitis b
37	33	97.1	42	12	Q80QT6	Q80qt6 hepatitis b
38	33	97.1	42	12	Q80QT4	Q80qt4 hepatitis b
39	33	97.1	42	12	Q80QT2	Q80qt2 hepatitis b
40	33	97.1	42	12	Q80QT0	Q80qt0 hepatitis b
41	33	97.1	42	12	Q80QS8	Q80qs8 hepatitis b
42	33	97.1	42	12	Q80QS6	Q80qs6 hepatitis b
43	33	97.1	42	12	Q80QS4	Q80qs4 hepatitis b
44	33	97.1	42	12	Q80QS2	Q80qs2 hepatitis b
45	33	97.1	42	12	Q80QS0	Q80qs0 hepatitis b

## ALIGNMENTS

RESULT 1

Q7YVW4	PRELIMINARY;	PRT;	44	AA.
AC Q7YVW4;				
DT 01-OCT-2003 (TREMBLrel. 25, Created)				
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)				
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE Hypothetical protein.				
GN TB927.2.920.				
OS Trypanosoma brucei.				
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.				
OX NCBI_TaxID=5691;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=Gutatio10.1;				
RA El-Sayed N.M.A., Ghedin E., Song J., Macleod A., Bringaud F.,				
RA Larkin C., Wanless D., Peterson J., Hou L., Taylor S., Tweedie A.,				
RA Biteau N., Khalak H.G., Lin X., Mason T., Hannick L., Caler E.,				
RA Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,				
RA Van Aken S., Utterback T., Haas B., Koo H.L., Umayam L., Suh B.,				
RA Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Feldblyum T.,				
RA Salzborg S., Tait A., Turner M.R., Ullu E., White O., Melville S.,				
RA Adams M.D., Fraser C.M., Donelson J.E.;				
RT "The sequence and analysis of Trypanosoma brucei chromosome II.";				
RL Nucleic Acids Res. 0:0-0(2003).				
DR EMBL; AF017167; AAQ15564.1; --				
KW Hypothetical protein.				
SQ SEQUENCE 44 AA; 4912 MW; 8B51647E5A860A64 CRC64;				

Query Match 100.0%; Score 34; DB 5; Length 44;

Best Local Similarity 100.0%; Pred. No. 6.5; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0;

QY 1 CTCVP 5

Db 14 CTCVP 18

RESULT 2

```

Q7YVU3
ID Q7YVU3 PRELIMINARY; PRT; 44 AA.
AC Q7YVU3; 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
GN TB927.2.1280.
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUta10.1;
RA El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Bringaard F.,
RA Larkin C., Wanless D., Peterson J., Hou L., Taylor S., Tweedie A.,
RA Bateau N., Khalak H.G., Lin X., Mason T., Hannick L., Caler E.,
RA Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,
RA Van Aken S., Uterback T., Haas B., Koo H.L., Umayam L., Suh B.,
RA Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Feldblum T.,
RA Salzberg S., Tait A., Turner M.R., Ullu E., White O., Melville S.,
RA Adams M.D., Fraser C.M., Donelson J.E.;
RA "The sequence and analysis of Trypanosoma brucei chromosome II.";
RL Nucleic Acids Res. 0:0-0(2003).
DR EMBL; AE017167; AA015588.1; -.
KW Hypothetical protein.
SQ SEQUENCE 44 AA; 4840 MW; 8B51647CD0860A64 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 14 CTCVP 18

RESULT 3
Q9LRE1 PRELIMINARY; PRT; 84 AA.
ID Q9LRE1
AC Q9LRE1; 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE S locus protein 11-26 (Fragment).
GN SF11-26.
OS Brassica campestris (field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S26(2-10);
RA Watanabe M., Ito A., Takada Y., Nimomiya C., Kakizaki T., Takahata Y.,
RA Hatakeyama K., Hinata K., Suzuki G., Takasaki T., Satta Y., Shiba H.,
RA Takayama S., Isogai A.;
RA "Highly divergent sequences of the pollen self-incompatibility (S)
RT gene in class-I S haplotypes of Brassica campestris (syn. rapa) L.";
RL FEBS Lett. 473:139-144(2000).
DR EMBL; AB039755; BAA96393.1; -.
FT NON_TER 1 1
FT TER 1 1
SQ SEQUENCE 84 AA; 9469 MW; B34D639503CEC6A7 CRC64;

Query Match 100.0%; Score 34; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 65 CTCVP 69

```

```

RESULT 4
Q81632 PRELIMINARY; PRT; 106 AA.
ID Q81632
AC Q81632; 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN PFL0065W.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shailom S.J., Suh B., Peterson J., Angiuoli S.,
RA Perteira M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McPadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RA "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014844; AAN36102.1; -.
KW Hypothetical protein.
SQ SEQUENCE 106 AA; 12267 MW; 6C6B54D391918E0A CRC64;

Query Match 100.0%; Score 34; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 22 CTCVP 26

RESULT 5
Q80NT4 PRELIMINARY; PRT; 121 AA.
ID Q80NT4
AC Q80NT4; 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE S protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrod viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLD2235;
RA Gandhe S.S., Chadha M.S., Arankalle V.A.;
RA "Clinical manifestations and HBV genotypes and serotypes in western
RT India.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF492222; AA084681.1; -.
GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
FT NON_TER 1 1
FT TER 1 1
SQ SEQUENCE 121 AA; 13138 MW; C6E5C4FB7B944859 CRC64;

Query Match 100.0%; Score 34; DB 12; Length 121;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

```

Db 104 CTCVP 108

|||||

## RESULT 6

Q96QM2 PRELIMINARY; PRT; 169 AA.

AC Q96QM2 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 25, Last sequence update)

DE Tissue inhibitor of metalloproteinase 1 (Brythroid potentiating activity, collagenase inhibitor).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC007097; AAH07097.1; -.

DR GO; GO:0005578; C:extracellular matrix; IEA.

DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.

DR InterPro; IPR001820; TIMP.

DR InterPro; IPR008993; TIMP\_like.

DR Pfam; PF00965; TIMP; 1.

DR SMART; SM00206; NTR; 1.

DR PROSITE; PS00288; TIMP; 1.

SQ SEQUENCE 169 AA; 18847 MW; 6C164206C87D815C CRC64;

Query Match 100.0%; Score 34; DB 4; Length 169;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 24 CTCVP 28

|||||

## RESULT 7

Q8K599 PRELIMINARY; PRT; 196 AA.

AC Q8K599;

DT 01-OCT-2002 (TREMELrel. 22, Created)

DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)

DE Interleukin 27A precursor.

GN IL17D OR IL27A.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Hadj-Slimane R.; Bobe P.;

RT "Interleukin 27A (IL27A); a newly identified cytokine.";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF502584; AAM33382.1; -.

DR MGD; MGI:2446510; IL17d.

KW SIGNAL.

FT SIGNAL.

SQ SEQUENCE 196 AA; 21124 MW; C350DFE028ABFC16 CRC64;

Query Match 100.0%; Score 34; DB 11; Length 196;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 165 CTCVP 169

|||||

## RESULT 8

Q8TAD2 PRELIMINARY; PRT; 202 AA.

AC Q8TAD2;

DT 01-JUN-2002 (TREMELrel. 21, Created)

DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)

DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)

DE Interleukin 27 precursor (IL-17D) (Interleukin 17D).

GN IL27.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Hadj-Slimane R.; Bobe P.;

RT "Interleukin 27 (IL27); a newly identified cytokine.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Hromas R.A.; Starnes T.T.;

RT "IL-17D, A Novel Member of the IL-17 Family, Stimulates Cytokine Production and Inhibits Hematopoiesis.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Gilbert J.M.; Gorman D.M.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY078238; AAL86911.1; -.

DR EMBL; AF479775; AAM12734.1; -.

DR EMBL; AF458062; AAM77566.1; -.

DR EMBL; BC036243; AAH36243.1; -.

DR Genew; HGNC:5984; IL17D.

KW SIGNAL.

FT SIGNAL.

SQ SEQUENCE 202 AA; 21893 MW; D171C5FB2DD039C3 CRC64;

Query Match 100.0%; Score 34; DB 4; Length 202;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 167 CTCVP 171

|||||

## RESULT 9

Q8K4C4 PRELIMINARY; PRT; 205 AA.

AC Q8K4C4;

DT 01-OCT-2002 (TREMELrel. 22, Created)

DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)

DE Interleukin 27 precursor (IL-17D) (Interleukin 17D).

GN IL17D.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Gilbert J.M.; Gorman D.M.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF458063; AAM77567.1; -.

DR MGD; MGI:2446510; IL17d.

```
SQ SEQUENCE 205 AA; 22390 MW; 6705746EF013318D CRC64;
Query Match 100.0%; Score 34; DB 11; Length 205;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 174 CTCVP 178

RESULT 10
Q96RY6 PRELIMINARY; PRT; 292 AA.
AC Q96RY6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN GS114.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
RL EMBL: AE006639; AAK61287.1; -.
KW Hypothetical protein.
SQ SEQUENCE 292 AA; 31183 MW; 785679B90314ABFA CRC64;

Query Match 100.0%; Score 34; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 160 CTCVP 164

RESULT 11
Q9GRG2 PRELIMINARY; PRT; 400 AA.
AC Q9GRG2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenoloxidase activating factor.
GN PPAF.
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Psocoptera;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Larva;
RX MEDLINE=20467200; PubMed=11012672;
RA Kwon T.H., Kim M.S., Choi H.W., Joo C.H., Cho M.Y., Lee B.L.;
RA "A maquerade-like serine proteinase homologue is necessary for
RT phenoloxidase activity in the coleopteran insect, Holotrichia
RT glomphalia larvae.";
RL Eur. J. Biochem. 267:6188-6195(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
KW HSP7; P00763; IDPO.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR
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DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 400 AA; 43754 MW; DEB882CB715D7D97 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 65 CTCVP 69

RESULT 12
Q8MSX5 PRELIMINARY; PRT; 487 AA.
AC Q8MSX5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE L013435P.
GN CRB OR CG6383.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Psocoptera;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarino H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY118509; AAM49878.1; -.
RL FlyBase; FBgn0000368; crb.
DR GO; GO:0016324; C:apical plasma membrane; NAS.
DR GO; GO:0016327; C:apicolateral plasma membrane; IDA.
DR GO; GO:0007163; P:establishment and/or maintenance of cell po. ; IMP.
DR GO; GO:0016332; P:establishment and/or maintenance of polarit. ; IMP.
DR GO; GO:0016334; P:establishment and/or maintenance of polarit. ; IMP.
DR GO; GO:0045494; P:photoreceptor maintenance; IMP.
DR GO; GO:0042052; P:rhabdome development; NAS.
DR GO; GO:0045186; P:zonula adherens assembly; IMP.
DR GO; GO:0045218; P:zonula adherens maintenance; IMP.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00008; EGF; 8.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 7.
DR
```



DR PROSITE; PS01186; EGF\_2; 6.  
 DR PROSITE; PS01187; EGF\_CA; 4.  
 DR PROSITE; PS50025; LAM\_G\_DOMAIN; 1.  
 KW EGF-like domain.  
 SQ SEQUENCE 487 AA; 52498 MW; C69E5B14E36B3D22 CRC64;  
 Query Match 100.0%; Score 34; DB 5; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVP 5  
 Db 241 CTCVP 245  
 |||||  
 RESULT 13  
 Q98201 ID Q98201 PRELIMINARY; PRT; 579 AA.  
 AC Q98201;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE MC0331.  
 GN MC0331.  
 OS Molluscum contagiosum virus subtype 1 (MCV1).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Molluscipoxvirus.  
 OX NCBI\_TaxID=10280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96325459; PubMed=8670425;  
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G., Moss B.;  
 RT "Genome sequence of a human tumorigenic poxvirus: Prediction of  
 RT specific host response-evasion genes."; Science 273:813-816(1996).  
 RL Science 273:813-816(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G., Moss B.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U60315; AAC55161.1; -.  
 DR PIR; T30635; T30635.  
 DR IncePro; IPR007110; Ig-like.  
 SQ SEQUENCE 579 AA; 62626 MW; A37930DF92D311A3 CRC64;  
 Query Match 100.0%; Score 34; DB 12; Length 579;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVP 5  
 Db 63 CTCVP 67  
 |||||  
 RESULT 14  
 Q80V54 ID Q80V54 PRELIMINARY; PRT; 608 AA.  
 AC Q80V54;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE I300015B04Rik protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=FVB/N; TISSUE=Breast tumor;  
 RC Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC043473; AAH43473.1; -.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR006552; VC\_out.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00008; EGF; 3.  
 DR Pfam; PF00093; VWC; 3.  
 DR SMART; SM00181; EGF; 4.  
 DR SMART; SM00179; EGF\_CA; 3.  
 DR SMART; SM00214; VWC; 3.  
 DR SMART; SM00215; VWC\_out; 3.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; VWF\_C\_1; 2.  
 DR PROSITE; PS01208; VWF\_C\_2; 2.  
 DR PROSITE; PS01208; VWF\_C\_2; 2.  
 SQ SEQUENCE 608 AA; 64109 MW; 72E7136A82FF764F CRC64;  
 Query Match 100.0%; Score 34; DB 11; Length 608;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCVP 5  
 Db 486 CTCVP 490  
 |||||  
 RESULT 15  
 Q8NEJ2 ID Q8NEJ2 PRELIMINARY; PRT; 646 AA.  
 AC Q8NEJ2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Similar to solute carrier family 4, sodium bicarbonate cotransporter, member 4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC030977; AAH30977.1; -.

DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005452; F:inorganic anion exchanger activity; IEA.  
 DR GO; GO:0006820; P:anion transport; IEA.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRANSPORT.  
 DR TIGREMS; TIGR00834; ae; 1.  
 SQ SEQUENCE 646 AA; 72048 MW; 285DSE23C540A516 CRC64;

Query Match 100.0%; Score 34; DB 4; Length 646;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
 |||||  
 Db 583 CTCVP 587

Search completed: April 8, 2004, 11:16:20  
 Job time : 21.5556 secs



F1-23/Domain: signal sequence #status predicted <SIG>  
 F124-206/Product: metalloproteinase inhibitor 1 #status predicted <MAT>  
 F124-93,26-122,36-147,150-168,155-160,168-188/Disulfide bonds: #status predicted  
 F153,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 1; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
 |||||  
 Db 24 CTCVP 28

RESULT 3  
 ZYHUEP

metallopeptidase tissue inhibitor 1 precursor [validated] - human  
 N/Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibitor  
 C/Species: Homo sapiens (man)  
 C/Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000  
 C/Accession: A93372; A93363; A20595; A35826; A48417; S20318; S15872; I52912; S66  
 R/Docherty, A.J.P.; Lyons, A.; Smith, B.J.; Wright, E.M.; Stephens, P.E.; Harris, T.J.R.  
 Nature 318, 66-69, 1985  
 A/Title: Sequence of human tissue inhibitor of metalloproteinases and its identity to ex  
 A/Reference number: A93372; MUID:86040463; PMID:3903517  
 A/Accession: A93372  
 A/Molecule type: mRNA  
 A/Residues: 1-207 <DOC>  
 A/Cross-references: GB:X03124; NID:G37182; PIDN:CAA26902.1; PID:G37183  
 R/Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.  
 Nature 315, 768-771, 1985  
 A/Title: Molecular characterization and expression of the gene encoding human erythroid  
 A/Reference number: A93363; MUID:85240567; PMID:3839290  
 A/Accession: A93363  
 A/Molecule type: mRNA  
 A/Residues: 1-207 <GAS>  
 R/Germichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, H.G.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 2407-2411, 1986  
 A/Title: Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.  
 A/Reference number: A23534; MUID:86205964; PMID:3010309  
 A/Accession: A23534  
 A/Molecule type: mRNA  
 A/Residues: 1-207 <CAR>  
 A/Cross-references: GB:M12670; NID:G182482; PIDN:AAA52436.1; PID:G182483  
 A/Note: parts of this sequence were confirmed by protein sequencing  
 A/Note: carbohydrate binding sites were determined  
 R/Stricklin, G.P.; Welgus, H.G.  
 J. Biol. Chem. 258, 12252-12258, 1983  
 A/Title: Human skin fibroblast collagenase inhibitor.  
 A/Reference number: A20595; MUID:84032401; PMID:6313647  
 A/Accession: A20595  
 A/Molecule type: protein  
 A/Residues: 24-44, 'L', 46 <STR>  
 A/Note: six disulfide bonds are present  
 R/Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K.  
 DNA Cell Biol. 9, 479-485, 1990  
 A/Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.  
 A/Reference number: A35826; MUID:91025550; PMID:2171551  
 A/Accession: A35826  
 A/Molecule type: mRNA  
 A/Residues: 1-207 <RAP>  
 R/Van Ranst, M.; Norga, K.; Masure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van  
 Cytokine 3, 231-239, 1991  
 A/Title: The cytokine-protease connection: identification of a 96-kD THP-1 gelatinase an  
 A/Reference number: A48417; MUID:91355647; PMID:1653055  
 A/Accession: A48417  
 A/Molecule type: protein  
 A/Residues: 'X', 25, 'X', 27-35, 'X', 37-52 <VAN>  
 A/Experimental source: monocytic cell line THP-1  
 A/Note: sequence modified after extraction from NCBI backbone  
 A/Note: sequence incorrectly identified as 96k gelatinase  
 R/Osthues, A.; Knaeuper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.

FBBS Lett. 296, 16-20, 1992  
 A/Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP  
 A/Reference number: S20318; MUID:92111776; PMID:1730286  
 A/Accession: S20318  
 A/Molecule type: protein  
 A/Residues: 'X', 25, 'X', 27-35, 'X', 37-38 <OST>  
 A/Experimental source: rheumatoid synovial fluid  
 R/Opdenakker, G.; Masure, S.; Proost, P.; Billiau, A.; van Damme, J.  
 FBBS Lett. 284, 73-78, 1991  
 A/Title: Natural human monocyte gelatinase and its inhibitor.  
 A/Reference number: S15872; MUID:91285112; PMID:1647974  
 A/Accession: S15872  
 A/Molecule type: protein  
 A/Residues: 'X', 25, 'X', 27-35, 'X', 37-42, 'X', 44, 'X', 46, 'X', 48-51 <FEB>  
 A/Experimental source: peripheral blood monocytes  
 R/Williamson, R.A.; Marston, F.A.O.; Angal, S.; Koklitis, P.; Panico, M.; Morris, H.R.;  
 Biochem. J. 268, 267-274, 1990  
 A/Title: Disulfide bond assignment in human tissue inhibitor of metalloproteinases (TIM  
 A/Reference number: A38978; MUID:90303199; PMID:2163605  
 A/Contents: annotation; disulfide bonds  
 R/Opbrock, A.; Kenney, M.C.; Brown, D.  
 Curr. Eye Res. 12, 877-883, 1993  
 A/Title: Characterization of a human corneal metalloproteinase inhibitor (TIMP-1).  
 A/Reference number: I52912; MUID:94123576; PMID:7507419  
 A/Accession: I52912  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-207 <RES>  
 A/Cross-references: GB:S68252; NID:G545022; PIDN:AAI4009.1; PID:G4261709  
 R/Triebl, S.; Blaeser, J.; Gote, T.; Pelz, G.; Schueren, E.; Schmitt, M.; Techesche, H.  
 Eur. J. Biochem. 231, 714-719, 1995  
 A/Title: Evidence for the tissue inhibitor of metalloproteinases-1 (TIMP-1) in human pol  
 A/Reference number: S66461; MUID:95377303; PMID:7649172  
 A/Accession: S66461  
 A/Molecule type: protein  
 A/Residues: 24-38 <TRI>  
 A/Experimental source: polymorphonuclear leukocytes  
 C/Comment: This protein, found in a variety of body fluids, complexes with metalloprote  
 S-specific, stimulating the growth and differentiation of only human and murine erythro  
 C/Comment: The remarkable heat stability of this protein may be due to disulfide bond  
 C/Genetics:  
 A/Gene: GDB:TIMP1; CLGI; TIMP  
 A/Cross-references: GDB:119615; OMIM:305370  
 A/Map position: Xp11.3-Xp11.23  
 C/Superfamily: metalloproteinase inhibitor  
 F/1-23/Domain: signal sequence #status predicted <SIG>  
 F/24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>  
 F/24-93,26-122,36-147,150-168,168-189/Disulfide bonds: #status experimental  
 F/53,101/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 34; DB 1; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5  
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 Db 24 CTCVP 28

RESULT 4  
 A35685  
 metalloproteinase inhibitor 1 precursor - bovine  
 N/Alternate names: cartilage-derived neovascularization inhibitor; TIMP-1; tissue inhib  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 21-Sep-1990 #sequence revision 12-Apr-1996 #text\_change 18-Jun-1999  
 C/Accession: A35685; B29712; A34833; I46979  
 R/Freudenstein, J.; Wagner, S.; Luck, R.M.; Einspanier, R.; Scheit, K.H.  
 Biochem. Biophys. Res. Commun. 171, 250-256, 1990  
 A/Title: mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression  
 A/Reference number: A35685; MUID:90365711; PMID:2393392  
 A/Accession: A35685  
 A/Molecule type: mRNA

A:Residues: 1-207 <PRE>  
A:Cross-references: GB:M60073; NID:G163760; PIDN:AAA30784.1; PID:G163761  
A:Experimental source: ovary cDNA library  
R:De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.  
J. Biol. Chem. 264, 17445-17453, 1989  
A:Title: Purification and characterization of two related but distinct metalloproteinase  
A:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor  
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted  
A:Accession: B34468  
A:Molecule type: protein  
A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P' <DEC>  
A:Experimental source: culture medium of aortic endothelial cells  
R:Kaczorek, M.; Honore, N.; Ribes, V.; Dehoux, P.; Cornet, P.; Cartwright, T.; Strecek,  
Bio/Technology 5, 595-598, 1987  
A:Title: Molecular cloning and synthesis of biologically active human tissue inhibitor o  
A:Reference number: A34468; MUID:90008914; PMID:2551903  
A:Accession: B34468  
A:Molecule type: protein  
A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P' <DEC>  
A:Experimental source: culture medium of fibroblastic BC 21 cells  
A:Note: protein inhibits angiogenesis  
R:Moses, M.A.; Sudhalter, J.; Langer, R.  
Science 248, 1408-1410, 1990  
A:Title: Identification of an inhibitor of neovascularization from cartilage.  
A:Reference number: A34833; MUID:90288433; PMID:1694043  
A:Accession: A34833  
A:Molecule type: protein  
A:Residues: 24-51 <MOS>  
A:Experimental source: cartilage  
R:Sato, T.; Kobayashi, K.; Yamashita, S.; Kikuchi, M.; Sendai, Y.; Hoshi, H.  
Biol. Reprod. 50, 835-844, 1994  
A:Title: Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and ovidu  
A:Reference number: I46979; MUID:94257757; PMID:8199264  
A:Accession: I46979  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-207 <SAT>  
A:Cross-references: GB:S70841; NID:G546973; PIDN:AAB30892.1; PID:G546974  
C:Function:  
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met  
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating  
A:Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent  
A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>  
F:24-93, 26-122, 36-147, 150-197, 155-160, 168-189/Disulfide bonds: #status predicted  
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVP 5  
Db 24 CTCVP 28

RESULT 5  
J4303  
matrix metalloproteinase-1 tissue inhibitor - baboon  
C:Species: Papio sp. (baboon)  
C>Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 16-Jul-1999  
C:Accession: J4303  
R:Forough, R.; Nikkari, S.T.; Hasenstab, D.; Lea, H.; Clowes, A.W.  
Gene 163, 267-271, 1995  
A:Title: Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of  
A:Reference number: J4303; MUID:96011646; PMID:7590279  
A:Accession: J4303  
A:Molecule type: mRNA  
A:Residues: 1-207 <FOR>  
A:Cross-references: GB:I37295; NID:G561545; PIDN:AAA99943.1; PID:G561546  
A:Experimental source: smooth muscle cell

C:Comment: This protein, a member of the tissue inhibitor of matrix metalloproteinase fa  
se and influences the proteinase activity. It has a role as a physiological molecule fo  
C:Genetics:  
A:Gene: timp-1  
C:Superfamily: metalloproteinase inhibitor  
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor  
F:53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVP 5  
Db 24 CTCVP 28

RESULT 6  
I46964  
metalloproteinase tissue inhibitor 1 precursor [similarity] - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 19-Jan-2001  
C:Accession: I46964  
R:Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.  
Endocrinology 134, 344-352, 1994  
A:Title: Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases: c  
eal tissue.  
A:Reference number: I46964; MUID:94102210; PMID:8275949  
A:Accession: I46964  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-207 <SMI>  
A:Cross-references: GB:S67450; NID:G456989; PIDN:AAB29472.1; PID:G456990  
C:Superfamily: metalloproteinase inhibitor

Query Match 100.0%; Score 34; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVP 5  
Db 24 CTCVP 28

RESULT 7  
I47061  
collagenase inhibitor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 16-Jul-1999  
C:Accession: I47061  
R:Tanaka, T.; Andoh, N.; Takeya, T.; Sato, E.  
Mol. Cell. Endocrinol. 83, 65-71, 1992  
A:Title: Differential screening of ovarian cDNA libraries detected the expression of the  
A:Reference number: I47061; MUID:92201478; PMID:1312961  
A:Accession: I47061  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-207 <TAN>  
A:Cross-references: GB:S96211; NID:G247729; PIDN:AAB21865.1; PID:G247730  
C:Superfamily: metalloproteinase inhibitor

Query Match 100.0%; Score 34; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVP 5  
Db 24 CTCVP 28

RESULT 8  
A43429  
metalloproteinase inhibitor 3 precursor - chicken



J. Mol. Evol. 29, 314-327, 1989  
A:Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpurus  
A:Reference number: A40136; MUID:90112459; PMID:2514273  
A:Accession: A40136  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-114 <DEL>  
A:Cross-references: GB:1X17530; NID:gl0225; PID:g667061  
A:Accession: B40136  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE>  
A:Accession: C40136  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 'K',747-821,898-978 <DE3>  
R:Hurch, D.A.; Andrews, M.E.; Raff, R.A.  
Science 237, 1487-1490, 1987  
A:Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.  
A:Reference number: A29316; MUID:87319677; PMID:3498216  
A:Accession: A29316  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260  
R:Hunt, L.T.; Barker, W.C.  
FASEB J. 3, 1760-1764, 1989  
A:Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.  
A:Reference number: A43131; MUID:89196806; PMID:2784773  
A:Contents: annotation  
C:Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-1064/Product: fibropellin I #status predicted <FIB>  
F:23-54/Domain: EGF homology <EG01>  
F:57-175/Domain: C1r/C1s repeat homology <C1R>  
F:180-211/Domain: EGF homology <EG02>  
F:218-249/Domain: EGF homology <EG03>  
F:256-287/Domain: EGF homology <EG04>  
F:294-325/Domain: EGF homology <EG05>  
F:332-363/Domain: EGF homology <EG06>  
F:370-401/Domain: EGF homology <EG07>  
F:408-439/Domain: EGF homology <EG08>  
F:446-477/Domain: EGF homology <EG09>  
F:484-515/Domain: EGF homology <EG10>  
F:522-553/Domain: EGF homology <EG11>  
F:560-591/Domain: EGF homology <EG12>  
F:598-629/Domain: EGF homology <EG13>  
F:636-667/Domain: EGF homology <EG14>  
F:674-705/Domain: EGF homology <EG15>  
F:712-743/Domain: EGF homology <EG16>  
F:750-781/Domain: EGF homology <EG17>  
F:788-819/Domain: EGF homology <EG18>  
F:826-857/Domain: EGF homology <EG19>  
F:864-895/Domain: EGF homology <EG20>  
F:902-933/Domain: EGF homology <EG21>  
F:936-1064/Region: avidin-like  
F:23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27  
57,451-466,468-477,484-495/Disulfide bonds: #status predicted  
F:489-504,506-515,522-533,527-542,544-553,560-571,598-609,603-618,620-62  
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Disul

Query Match 100.0%; Score 34; DB 2; Length 1064;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVP 5  
DB 542 CTCVP 546  
RESULT 13  
PC7034

Na+ bicarbonate cotransporter - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: PC7034  
R:Thevenod, F.; Roussa, E.; Schmitt, B.M.; Romero, M.F.  
Biochem. Biophys. Res. Commun. 264, 291-298, 1999  
A:Title: Cloning and immunolocalization of a rat pancreatic Na+ bicarbonate cotransporter  
A:Reference number: PC7034; MUID:99458660; PMID:10527880  
A:Accession: PC7034  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1079 <THE>  
A:Cross-references: GB:AF107265; NID:g6523792; PID:g6523793  
C:Genetics:  
A:Gene: nbc  
C:Superfamily: band 3 anion transport protein  
Query Match 100.0%; Score 34; DB 2; Length 1079;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVP 5  
DB 627 CTCVP 631  
RESULT 14  
TI4274  
versican precursor, splice form V2 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 05-May-2000  
C:Accession: TI4274  
R:Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.  
J. Biol. Chem. 273, 15758-15764, 1998  
A:Title: Versican V2 is a major extracellular matrix component of the mature bovine brain  
A:Reference number: Z17954; MUID:98288320; PMID:9624174  
A:Accession: TI4274  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-1643 <SCH>  
A:Cross-references: EMBL:AF060458; NID:g32533303; PID:g32533304; PIDN:AAC24360.1  
A:Experimental source: brain  
C:Keywords: glycoprotein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-1643/Product: versican, splice form V2 #status predicted <MAT>  
F:57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 100.0%; Score 34; DB 2; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCVP 5  
DB 1360 CTCVP 1364  
RESULT 15  
A35672  
crumbs protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 21-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_change 21-Jul-2003  
C:Accession: A35672  
R:Teppass, U.; Theres, C.; Knust, E.  
Cell 61, 787-799, 1990  
A:Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila  
A:Reference number: A35672; MUID:90263104; PMID:2344615  
A:Accession: A35672  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2139 <TEP>  
A:Cross-references: GB:M33753  
A:Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue  
C:Genetics:

A:Gene: FlyBase:Crb  
 A:Cross-references: FlyBase:FBgn000368  
 C:Keywords: transmembrane protein  
 F:352-385/Domain: EGF homology <EGX1>  
 F:392-424/Domain: EGF homology <EGF1>  
 F:691-722/Domain: EGF homology <EGF>  
 F:767-799/Domain: EGF homology <EGF3>  
 F:1878-1914/Domain: EGF homology <EGX2>

Query Match 100.0%; Score 34; DB 2; Length 2139;  
 Best Local Similarity 100.0%; Pred. NO. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
 Db 1903 CTCVP 1907

Search completed: April 8, 2004, 11:18:08  
 Job time : 7.80556 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:00:44 ; Search time 4.16667 Seconds  
(without alignments)  
62.484 Million cell updates/sec

Title: US-09-753-139c-8  
Perfect score: 34  
Sequence: 1 CTCVP 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	206	1 TIM1_RABIT	P20614 oryctolagus
2	34	100.0	207	1 TIM1_BOVIN	P20414 bos taurus
3	34	100.0	207	1 TIM1_HORSE	O02722 equus caball
4	34	100.0	207	1 TIM1_HUMAN	P01033 homo sapien
5	34	100.0	207	1 TIM1_PAPCY	P49061 papio cynoc
6	34	100.0	207	1 TIM1_PIG	P35624 sus scrofa
7	34	100.0	207	1 TIM1_SHEEP	P50122 ovis aries
8	34	100.0	212	1 TIM3_CHICK	P26552 gallus gall
9	34	100.0	862	1 PGCY_MACNE	Q28858 macaca neme
10	34	100.0	1064	1 FBPI_STRPU	P10079 strongyloce
11	34	100.0	2139	1 CRB_DROME	P10040 drosophila
12	34	100.0	3381	1 PGCY_BOVIN	P81282 bos taurus
13	34	100.0	3396	1 PGCY_HUMAN	P13611 homo sapien
14	33	97.1	226	1 VMSA_HBEVO	P31873 hepatitis b
15	33	97.1	226	1 VMSA_HBEVD	P31868 hepatitis b
16	33	97.1	226	1 VMSA_HBEVN	P30019 hepatitis b
17	33	97.1	226	1 VMSA_HBEVS	P31869 hepatitis b
18	33	97.1	389	1 VMSA_HBEVA	P24025 hepatitis b
19	33	97.1	389	1 VMSA_HBEVI	P17397 hepatitis b
20	33	97.1	389	1 VMSA_HBEVJ	P17398 hepatitis b
21	33	97.1	389	1 VMSA_HBEVL	P12911 hepatitis b
22	33	97.1	389	1 VMSA_HBEVO	P17399 hepatitis b
23	33	97.1	389	1 VMSA_HBEVW	P03142 hepatitis b
24	33	97.1	389	1 VMSA_HBEVY	P03138 hepatitis b
25	33	97.1	389	1 VMSA_HBEVZ	P03139 hepatitis b
26	33	97.1	400	1 VMSA_HBEV2	P03141 hepatitis b
27	33	97.1	400	1 VMSA_HBEV4	P12934 hepatitis b
28	33	97.1	400	1 VMSA_HBEV9	P17101 hepatitis b
29	33	97.1	400	1 VMSA_HBEVP	Q02317 hepatitis b
30	33	97.1	400	1 VMSA_HBEVR	P03140 hepatitis b
31	33	97.1	400	1 VMSA_HBEVT	Q05496 hepatitis b
32	31	91.2	214	1 TIM3_SCYTO	Q9w684 scyllothinu
33	31	91.2	376	1 FA10_HOBST	P83370 hoptocephal

34	31	91.2	376	1 FA10_TROCA	P81428 tropidechis
35	31	91.2	570	1 FBPI_STRPU	P49013 strongyloce
36	31	91.2	666	1 MOD_DROME	P18105 drosophila
37	31	91.2	686	1 DLL4_MOUSE	Q9j171 mus musculu
38	31	91.2	1964	1 NTC4_MOUSE	P31695 mus musculu
39	31	91.2	2003	1 NTC4_HUMAN	Q99466 homo sapien
40	31	91.2	2524	1 NOTC_XENLA	P21783 xenopus lae
41	31	91.2	3562	1 PGCY_CHICK	Q90953 gallus gall
42	30	88.2	57	1 YC57_HAEIN	P44143 haemophilus
43	30	88.2	92	1 LCM_LOEMI	P80060 locusta mig
44	30	88.2	158	1 VGO9_HSV11	Q00163 ictalurid h
45	30	88.2	162	1 BAR2_CHIPA	P08725 chironomus

## ALIGNMENTS

### RESULT 1

TIMI_RABIT	STANDARD;	PRT;	206 AA.
AC P20614;			
DT 01-PEB-1991 (Rel. 17, Created)			
DT 01-PEB-1991 (Rel. 17, Last sequence update)			
DT 15-MAR-2004 (Rel. 43, Last annotation update)			
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).			
GN TIMP1.			
OS Oryctolagus cuniculus (Rabbit).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX NCBI_TaxID:9986;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=89214135; PubMed=2708356;			
RA Horowitz S., Dafni N., Shapiro D.L., Holm B.A., Notter R.H.,			
RA Quibie D.J.;			
RT "Hyperoxic exposure alters gene expression in the lung. Induction of			
RT the tissue inhibitor of metalloproteinases mRNA and other mRNAs.";			
RL J. Biol. Chem. 264:7092-7095(1989).			
CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)			
CC and irreversibly inactivates them.			
CC -!- SUBCELLULAR LOCATION: Secreted.			
CC -!- PTM: The activity of TIMP1 is dependent on the presence of			
CC disulfide bonds.			
CC -!- SIMILARITY: Belongs to the TIMP family.			
CC -!- SIMILARITY: Contains 1 NTR domain.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC the European Bioinformatics Institute. There are no restrictions on its			
CC use by non-profit institutions as long as its content is in no way			
CC modified and this statement is not removed. Usage by and for commercial			
CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC -----			
DR EMBL; J04712; AAA31478.1; -			
DR PIR; A33350; A33350.			
DR HSP; P01033; 1D2B.			
DR InterPro; IPR001820; TIMP.			
DR InterPro; IPR008993; TIMP_like.			
DR Pfam; PF00965; TIMP; 1.			
DR SMART; SM00206; NTR; 1.			
DR PROSITE; PS0189; NTR; 1.			
DR PROSITE; PS00288; TIMP; 1.			
DR Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;			
KW Signal.			
FT SIGNAL	1	23	METALLOPROTEINASE INHIBITOR 1.
FT CHAIN	24	206	NTR.
FT DOMAIN	24	147	BY SIMILARITY.
FT DISULFID	24	93	BY SIMILARITY.
FT DISULFID	26	122	BY SIMILARITY.
FT DISULFID	36	147	BY SIMILARITY.
FT DISULFID	150	196	BY SIMILARITY.
FT DISULFID	155	160	BY SIMILARITY.

FT DISULFID 168 188 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 206 AA; 22758 MW; 1839ABDE174EE9E CRC64;

Query Match 100.0%; Score 34; DB 1; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 7.4;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
 Db 24 CTCVP 28

RESULT 2  
 TIM1\_BOVIN STANDARD; PRT; 207 AA.  
 AC P20414; Q9TVB0;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Embryogenin-1) (EG-1).  
 GN TIMP1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 ON NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90365711; PubMed=2393392;  
 RA Freudenstein J., Wagner S., Luck R.M., Einspanier R., Scheit K.H.;  
 RT "mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue."  
 RL Biochem. Biophys. Res. Commun. 171:250-256(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94257757; PubMed=8199264;  
 RA Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.;  
 RT "Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct cells enhances in vitro development of bovine embryo."  
 RL Biol. Reprod. 50:835-844(1994).  
 RN [3]  
 RP SEQUENCE OF 25-191 FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RA Balcerzak D., Quereingesser L., Dixon W.T., Baracos V.E.;  
 RT "Involvement of fibroblasts and muscle cells in the expression of an extracellular proteolytic cascade in bovine skeletal muscle."  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP PRELIMINARY SEQUENCE OF 24-69.  
 RX MEDLINE=9008914; PubMed=2551903;  
 RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;  
 RT "Purification and characterization of two related but distinct metalloproteinase inhibitors secreted by bovine aortic endothelial cells."  
 RL J. Biol. Chem. 264:17445-17453(1989).  
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases) and irreversibly inactivates them.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of disulfide bonds.  
 CC -1- SIMILARITY: Belongs to the TIMP family.  
 CC -1- SIMILARITY: Contains 1 NTR domain.

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EMBL; M60073; AAA30784.1; -;  
 EMBL; S70841; AAB30892.1; -;  
 EMBL; AF144763; AAD30303.1; -;  
 PIR; A35685; A35685.  
 HSSP; P01033; IUEA.  
 DR InterPro; IPR001820; TIMP.  
 DR InterPro; IPR008993; TIMP\_like.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SMO0206; NTR; 1.  
 DR PROSITE; PS50189; NTR; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
 KW Signal.  
 FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.  
 FT CHAIN 24 207 NTR.  
 FT DOMAIN 24 147 BY SIMILARITY.  
 FT DISULFID 24 93 BY SIMILARITY.  
 FT DISULFID 26 122 BY SIMILARITY.  
 FT DISULFID 36 147 BY SIMILARITY.  
 FT DISULFID 150 197 BY SIMILARITY.  
 FT DISULFID 155 160 BY SIMILARITY.  
 FT DISULFID 168 189 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 207 AA; 23031 MW; B672BEE2E865F3F7 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 7.4;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
 Db 24 CTCVP 28

RESULT 3  
 TIM1\_HORSE STANDARD; PRT; 207 AA.  
 AC O02722;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).  
 GN TIMP1.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 ON NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cartilage;  
 RX MEDLINE=99074117; PubMed=9858406;  
 RA Richardson D.W., Dodge G.R.;  
 RT "Molecular characteristics of equine stromelysin and the tissue inhibitor of metalloproteinase 1."  
 RL Am. J. Vet. Res. 59:1557-1562(1998).  
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases) and irreversibly inactivates them (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of disulfide bonds (By similarity).  
 CC -1- SIMILARITY: Belongs to the TIMP family.  
 CC -1- SIMILARITY: Contains 1 NTR domain.

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CC DR EMBL; U95039; AAB53735.1; -
DR HSP; P01033; 1UEA.
DR InterPro; IPR001820; TIMP.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
DR PROSITE; PS0189; NTR; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 BY SIMILARITY.
FT DOMAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
FT CHAIN 24 147 NTR.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23046 MW; PD710DA98D168070 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
DB 24 CTCVP 28

RESULT 4
TIMP_HUMAN STANDARD; PRT; 207 AA.
ID P01033; Q14252; Q9UCU1;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Metalloprotease inhibitor 1 precursor (TIMP-1) (Erythroid
DE Potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases)
DE (Fibroblast collagenase inhibitor) (Collagenase inhibitor).
GN TIMP OR TIMP OR CLGI.
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=86040463; PubMed=3903517;
RX Doeherty A.J.P., Lyons A., Smith B.J., Wright E.M., Stephens P.E.,
RA Harris T.J.R., Murphy G., Reynolds J.J.;
RT "Sequence of human tissue inhibitor of metalloproteinases and its
RT identity to erythroid-potentiating activity.";
RL Nature 318:66-69 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85240567; PubMed=3839290;
RA Gasson J.C., Golde D.W., Kaufman S.E., Westbrook C.A., Hewick R.M.,
RA Kaufman R.J., Wong G.G., Temple P.A., Leary A.C., Brown E.L.,
RA Orr E.C., Clark S.C.;
RT "Molecular characterization and expression of the gene encoding human
RT erythroid-potentiating activity.";
RL Nature 315:768-771 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205964; PubMed=3010309;
RA Carmichael D.P., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,
RA Welgus H.G., Stricklin G.P.;
RT "Primary structure and cDNA cloning of human fibroblast collagenase
RT inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411 (1986).

[4]
RN SEQUENCE FROM N.A.
RP Kaczorek M., Honore N., Ribes V., Dehoux P., Cornet P., Cartwright T.,
RA Streeck R.E.;
RT "Molecular cloning and synthesis of biologically active human tissue
RT inhibitor of metalloproteinases in yeast.";
RL Biotechnology 5:595-598 (1987).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=91025550; PubMed=2171551;
RA Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,
RA Scheit K.H.;
RT "Characterization of three abundant mRNAs from human ovarian
RT granulosa cells.";
RL DNA Cell Biol. 9:479-485 (1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=94123576; PubMed=7507419;
RA Opbroek A., Kenney M.C., Brown D.;
RT "Characterization of a human corneal metalloproteinase inhibitor
RT (TIMP-1).";
RL Curr. Eye Res. 12:877-883 (1993).
RN [7]
RN SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP SEQUENCE OF 42-207 FROM N.A.
RA Matsuda T., Kohno K., Kuwano M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 1-40 FROM N.A.
RA Hardecastle A.J.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [10]
RP DISULFIDE BONDS, AND PARTIAL SEQUENCE.
RX MEDLINE=90303199; PubMed=2163605;
RA Williamson R.A., Martson F.A.O., Angal S., Koklitis P., Panico M.,
RA Morris H.R., Carne A.F., Smith B.J., Harris T.J.R., Freedman R.B.;
RT "Disulphide bond assignment in human tissue inhibitor of
RT metalloproteinases (TIMP).";
RL Biochem. J. 268:267-274 (1990).
RN [11]
RP SEQUENCE OF 24-38.
RC TISSUE=Synovial fluid;
RX MEDLINE=92111776; PubMed=1730286;
RA Othues A., Knauper V., Oberhoff R., Reinke H., Tschesche H.;
RT "Isolation and characterization of tissue inhibitors of
RT metalloproteinases (TIMP-1 and TIMP-2) from human rheumatoid synovial
RT fluid.";
RL FEBS Lett. 296:16-20 (1992).
RN [12]

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SEQUENCE OF 24-52.  
 RX MEDLINE=91355647; PubMed=1653055;  
 RA Van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,  
 RA Auwerx J., Van Damme J., Odenakker G.;  
 RT "The cytokine-protease connection: identification of a 96-kD THP-1  
 RT gelatinase and regulation by interleukin-1 and cytokine inducers.";  
 RL Cytokine 3:231-239(1991).  
 RN [13]  
 RN MUTAGENESIS.  
 RX MEDLINE=93041700; PubMed=1420137;  
 RA O'Shea M., Willenbrock F., Williamson R.A., Cockett M.I.,  
 RA Freedman R.B., Reynolds J.J., Docherty A.J.P., Murphy G.;  
 RT "Site-directed mutations that alter the inhibitory activity of the  
 RT tissue inhibitor of metalloproteinases-1: importance of the  
 RT N-terminal region between cysteine 3 and cysteine 13.";  
 RL Biochemistry 31:10146-10152(1992).  
 RN [14]  
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH MMP-3.  
 RX MEDLINE=97433330; PubMed=9288970;  
 RA Gomis-Ruth F.X., Maskos K., Betz M., Beigner A., Huber R., Suzuki K.,  
 RA Yoshida N., Nagase H., Brew K., Bournekov G.P., Bartunik H., Bode W.;  
 RT "Mechanism of inhibition of the human matrix metalloproteinase  
 RT stromelysin-1 by TIMP-1.";  
 RL Nature 389:77-81(1997).  
 RN [15]  
 RN STRUCTURE BY NMR OF 24-149.  
 RX MEDLINE=20090931; PubMed=10623524;  
 RA Wu B., Arumugam S., Gao G., Lee G.I., Semchenko V., Huang W.,  
 RA Brew K., Van Doren S.R.;  
 RT "NMR structure of tissue inhibitor of metalloproteinases-1 implicates  
 RT localized induced fit in recognition of matrix metalloproteinases.";  
 RL J. Mol. Biol. 295:257-268(2000).  
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATES THEM. ALSO MEDIATES ERYTHROPOIESIS IN  
 CC VITRO; BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE  
 CC GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID  
 CC PROGENITORS. KNOWN TO ACT ON MMP-1, MMP-2, MMP-3, MMP-7, MMP-8,  
 CC MMP-9, MMP-10, MMP-11, MMP-12, MMP-13 AND MMP-16. DOES NOT ACT ON  
 CC MMP-14.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of  
 CC disulfide bonds.  
 CC -1- SIMILARITY: Belongs to the TIMP family.  
 CC -1- SIMILARITY: Contains 1 NTR domain.  
 CC  
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 CC  
 DR EMBL; X03124; CAA26902.1; -  
 DR EMBL; M12670; AAS2436.1; -  
 DR EMBL; X02598; CAA26443.1; -  
 DR EMBL; M59906; AAG3234.1; -  
 DR EMBL; S68252; AAD14009.1; -  
 DR EMBL; BC000866; AAH00866.1; -  
 DR EMBL; D11139; BAA01913.1; -  
 DR EMBL; I47361; AAY5558.1; -  
 DR EMBL; A10416; CAA00898.1; -  
 DR PIR; A93372; ZYHUEP.  
 DR PDB; 1UEA; 25-NOV-98.  
 DR PDB; 1D2B; 22-DEC-99.  
 DR PDB; 1LQN; 05-JUN-02.  
 DR GlycoSuiteDB; P01033; -  
 DR Gnew; HGNC:11820; TIMP1.  
 DR MIM; 305370; -  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; TAS.  
 DR GO; GO:0008237; F:metalloproteinase activity; NAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
 DR InterPro; IPR001820; TIMP.  
 DR InterPro; IPR008993; TIMP\_like.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM00206; NTR; 1.  
 DR PROSITE; PS0189; NTR; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
 KW 3D-structure; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.  
 FT DOMAIN 24 147 NTR.  
 FT DISULFID 24 93  
 FT DISULFID 26 122  
 FT DISULFID 36 147  
 FT DISULFID 150 197  
 Query Match 100.0%; Score 34; DB 1; Length 207;  
 Best Local Similarity 100.0%; Pred. No 7.4; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTCVP 5  
 Db 24 CTCVP 28  
 RESULT 5  
 TIMP\_PAPCY STANDARD; PRT; 207 AA.  
 ID TIMP\_PAPCY AC P49061;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).  
 GN TIMP1.  
 OS Papio cynocephalus (Yellow baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Papio.  
 OC NCBI\_TaxID=9556;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Aorta;  
 RX MEDLINE=96011646; PubMed=7590279;  
 RA Porough R., Nikkari S.P., Hasenstab D., Lea H., Clowes A.W.;  
 RT "Cloning and characterization of a cDNA encoding the baboon tissue  
 RT inhibitor of matrix metalloproteinase-1 (TIMP-1).";  
 RL Gene 163:267-271(1995).  
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)  
 CC and irreversibly inactivates them.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of  
 CC disulfide bonds.  
 CC -1- SIMILARITY: Belongs to the TIMP family.  
 CC -1- SIMILARITY: Contains 1 NTR domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; L37295; AAA99943.1; -  
 DR HSSP; P01033; 1D2B.  
 DR InterPro; IPR001820; TIMP.  
 DR InterPro; IPR008993; TIMP\_like.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM00206; NTR; 1.  
 DR PROSITE; PS0189; NTR; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;

```

KW Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
FT DOMAIN 24 147 NTR.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23213 MW; 5AB4FDBEAB2ECDC CRC64;

Query Match 100.0%; Score 34; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
DB 24 CTCVP 28

RESULT 6
TIM1_PIG STANDARD; PRT; 207 AA.
AC P35624; Q9TTB3; Q9TTB9;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=92201478; PubMed=1312961;
RA Tanaka T., Andoh N., Takeya T., Sato E.;
RT "Differential screening of ovarian cDNA libraries detected the
RT expression of the porcine collagenase inhibitor gene in functional
RT corpora lutea.";
RL Mol. Cell. Endocrinol. 83:65-71(1992).
RN [2]
RP SEQUENCE OF 34-195 FROM N.A.
RA Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;
RT "Gene expression level of mmp3 and Timpi in intervertebral disc.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 37-144 FROM N.A.
RC TISSUE=Skin;
RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
RT "Cloning and sequencing of porcine TIMPs.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC and irreversibly inactivates them.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: The activity of TIMP1 is dependent on the presence of
CC disulfide bonds.
CC -!- SIMILARITY: Belongs to the TIMP family.
CC -!- SIMILARITY: Contains 1 NTR domain.
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CC -----
EMBL; S96211; AAB21865.1; -.

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DR EMBL; AF201726; AAF24348.1; -.
DR EMBL; AF156029; AAF17354.1; -.
DR PIR; I47061; I47061.
DR HSSP; P01033; 1UEA.
DR InterPro; IPR001820; TIMP.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00985; TIMP; 1.
DR SMART; SMO0206; NTR; 1.
DR PROSITE; PS00189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
FT DOMAIN 24 147 NTR.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 34 34 A -> P (IN REF. 2).
FT CONFLICT 37 37 S -> N (IN REF. 3).
FT CONFLICT 41 41 V -> F (IN REF. 2).
FT CONFLICT 59 59 K -> Q (IN REF. 1).
FT CONFLICT 86 86 T -> A (IN REF. 3).
FT CONFLICT 141 142 EI -> KT (IN REF. 3).
SQ SEQUENCE 207 AA; 23098 MW; B04895846B56BD0 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
DB 24 CTCVP 28

RESULT 7
TIM1_SHEEP STANDARD; PRT; 207 AA.
AC P50122;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN TIMP1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus luteum;
RX MEDLINE=94102210; PubMed=8275949;
RA Smith G.W., Goetz T.L., Anthony R.V., Smith M.P.;
RT "Molecular cloning of an ovine ovarian tissue inhibitor of
RT metalloproteinases: ontogeny of messenger ribonucleic acid expression
RT and in situ localization within preovulatory follicles and luteal
RT tissue.";
RL Endocrinology 134:344-352(1994).
CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC and irreversibly inactivates them.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: The activity of TIMP1 is dependent on the presence of
CC disulfide bonds.
CC -!- SIMILARITY: Belongs to the TIMP family.
CC -!- SIMILARITY: Contains 1 NTR domain.
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DR EMBL; S67450; AAB29472.1; -  
 DR PIR; I46964; I46964.  
 DR HSSP; P01033; IUEA.  
 DR InterPro; IPR001820; TIMP.  
 DR InterPro; IPR008993; TIMP\_like.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM00206; NTR; 1.  
 DR PROSITE; PS50189; NTR; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;  
 KW Signal.  
 FT SIGNAL 1 23 BY SIMILARITY.  
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.  
 FT DOMAIN 24 147 NTR.  
 FT DISULFID 24 93 BY SIMILARITY.  
 FT DISULFID 26 122 BY SIMILARITY.  
 FT DISULFID 36 147 BY SIMILARITY.  
 FT DISULFID 150 197 BY SIMILARITY.  
 FT DISULFID 155 160 BY SIMILARITY.  
 FT DISULFID 168 189 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 207 AA; 23057 MW; 133BCA2012F80E46 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 7.4;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
 Db 24 CTCVP 28

RESULT 8  
 ID TIM3 CHICK STANDARD; PRT; 212 AA.  
 AC P26652;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Metalloprotease inhibitor 3 precursor (TIMP-3) (Tissue inhibitor of  
 DE metalloproteases-3) (21 kDa protein of extracellular matrix).  
 GN TIMP3 OR IMP-3.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryonic fibroblast;  
 RX MEDLINE=92381050; PubMed=1512267;  
 RA Pavloff N., Staskus P.W., Kishanani N.S., Hawkes S.P.;  
 RT "A new inhibitor of metalloproteinases from chicken: ChIMP-3. A third  
 RT member of the TIMP family.";  
 RL J. Biol. Chem. 267:17321-17326(1992).  
 RN [2]  
 RP SEQUENCE OF 25-53.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=91093162; PubMed=1845973;  
 RA Staskus P.W., Nasirz F.R., Fallanck L.J., Hawkes S.P.;  
 RT "The 21-kDa protein is a transformation-sensitive metalloproteinase  
 RT inhibitor of chicken fibroblasts.";  
 RL J. Biol. Chem. 266:449-454(1991).  
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)  
 CC and irreversibly inactivates them. May form part of a tissue-

CC specific acute response to remodeling stimuli.  
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -1- SIMILARITY: Belongs to the TIMP family.  
 CC -1- SIMILARITY: Contains 1 NTR domain.  
 CC -----

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DR EMBL; M94531; AAA48813.1; -  
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 DR HSSP; P16035; IBR9.  
 DR InterPro; IPR001820; TIMP.  
 DR InterPro; IPR008993; TIMP\_like.  
 DR Pfam; PF00965; TIMP; 1.  
 DR SMART; SM00206; NTR; 1.  
 DR PROSITE; PS50189; NTR; 1.  
 DR PROSITE; PS00288; TIMP; 1.  
 KW Metalloprotease inhibitor; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 212 METALLOPROTEINASE INHIBITOR 3.  
 FT DOMAIN 25 144 NTR.  
 FT DISULFID 25 92 BY SIMILARITY.  
 FT DISULFID 27 119 BY SIMILARITY.  
 FT DISULFID 37 144 BY SIMILARITY.  
 FT DISULFID 146 193 BY SIMILARITY.  
 FT DISULFID 151 156 BY SIMILARITY.  
 FT DISULFID 164 185 BY SIMILARITY.  
 SQ SEQUENCE 212 AA; 24504 MW; 17F159ADE108D618 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5  
 Db 25 CTCVP 29

RESULT 9  
 ID PGCV MACNE STANDARD; PRT; 862 AA.  
 AC Q28858; Q28859; Q28860;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Versican core protein (Large fibroblast proteoglycan) (Chondroitin  
 DE sulfate proteoglycan core protein 2) (Fragments).  
 GN CSFG2.  
 OS Macaca nemestrina (Pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
 OC Cercopitheidae; Macaca.  
 OX NCBI\_TaxID=9545;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Aortic smooth muscle;  
 RX MEDLINE=95005762; PubMed=7921538;  
 RA Yao L.Y., Moody C., Schoenherr E., Wight T.N., Sandell L.J.;  
 RT "Identification of the proteoglycan versican in aorta and smooth  
 RT muscle cells by DNA sequence analysis, in situ hybridization and  
 RT immunohistochemistry.";  
 RL Matrix Biol. 14:213-225(1994).  
 CC -1- FUNCTION: May play a role in intercellular signaling and in  
 CC connecting cells with the extracellular matrix. May take part in  
 CC the regulation of cell motility, growth and differentiation. Binds  
 CC hyaluronan.  
 CC -1- SUBUNIT: Interacts with FBLN1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By







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DB          542 CTCVP 546

RESULT 11
CRB_DROME
ID CRB_DROME STANDARD; PRT; 2139 AA.
AC P10040;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Crumbs protein precursor (95P).
GN CRB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Oregon-R; TISSUE=Embryo;
RX MEDLINE=90263104; PubMed=2344615;
RA Tepas U., Theres C., Knust E.;
RT "Crumbs encodes an EGF-like protein expressed on apical membranes of
RT Drosophila epithelial cells and required for organization of
RT epithelia.";
RL Cell 61:787-799(1990).
RN [2]
SEQUENCE OF 1663-1955 FROM N.A.
RP TISSUE=Embryo;
RX MEDLINE=87218537; PubMed=3107985;
RA Knust E., Dietrich U., Tepas U., Bremer K.A., Weigel D.,
RA Vaessin H., Campos-Ortega J.A.;
RT "EGF homologous sequences encoded in the genome of Drosophila
RT melanogaster, and their relation to neurogenic genes.";
RL EMBO J. 6:761-766(1987).
CC -!- FUNCTION: May play a role in the development of epithelia,
CC possibly for the establishment and/or maintenance of cell
CC polarity. It may act as a signal.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: GLYCOPHYLORATED IN THE CYTOPLASMIC DOMAIN (POTENTIAL).
CC -!- SIMILARITY: Contains 29 EGF-like domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -----
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DR EMBL; M33753; AAA28428.1; ALT_SEQ.
DR EMBL; X05144; CAA28793.1; -.
DR PIR; A35672; A35672.
DR PIR; B26637; B26637.
DR HSP; P00740; IEDM.
DR FlyBase; FBgn000368; crb.
DR GO; GO:0016324; C:apical plasma membrane; NAS.
DR GO; GO:0016327; C:picolateral plasma membrane; IDA.
DR GO; GO:0007163; P:establishment and/or maintenance of cell po. . ; IMP.
DR GO; GO:0016332; P:establishment and/or maintenance of polarit. . ; IMP.
DR GO; GO:0016334; P:establishment and/or maintenance of polarit. . ; IMP.
DR GO; GO:0045494; P:photoreceptor maintenance; IMP.
DR GO; GO:0042052; P:rhodomeceptor development; NAS.
DR GO; GO:0045186; P:zonula adherens assembly; IMP.
DR GO; GO:0045218; P:zonula adherens maintenance; IMP.
DR InterPro; IPR001052; Aex_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002049; Laminin_EGF.

DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00008; EGF; 26.
DR Pfam; PF00054; laminin_G; 3.
DR PRINTS; PRO0010; EGFELOOD.
DR PRINTS; PRO0011; EGFLAMININ.
DR SMART; SM00179; EGF_CA; 11.
DR SMART; SM00282; LamG; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 15.
DR PROSITE; PS00022; EGF_1; 26.
DR PROSITE; PS01186; EGF_2; 17.
DR PROSITE; PS00026; EGF_3; 27.
DR PROSITE; PS01187; EGF_CA; 12.
DR PROSITE; PS00025; LAM_G_DOMAIN; 3.
KW Differentiation; Repeat; EGF-like domain; Transmembrane;
KW Glycoprotein; Signal; Phosphorylation.
FT SIGNAL 1 90
FT CHAIN 91 2139 CRUMBS PROTEIN.
FT DOMAIN 91 2084 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2085 2111 POTENTIAL.
FT DOMAIN 2112 2139 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 267 303 EGF-LIKE 1.
FT DOMAIN 306 343 EGF-LIKE 2.
FT DOMAIN 348 386 EGF-LIKE 3.
FT DOMAIN 388 425 EGF-LIKE 4.
FT DOMAIN 427 463 EGF-LIKE 5.
FT DOMAIN 464 500 EGF-LIKE 6.
FT DOMAIN 501 532 EGF-LIKE 7.
FT DOMAIN 545 581 EGF-LIKE 8.
FT DOMAIN 582 611 EGF-LIKE 9.
FT DOMAIN 609 646 EGF-LIKE 10.
FT DOMAIN 648 685 EGF-LIKE 11.
FT DOMAIN 687 723 EGF-LIKE 12.
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FT DOMAIN 802 838 EGF-LIKE 15.
FT DOMAIN 840 902 EGF-LIKE 16.
FT DOMAIN 904 940 EGF-LIKE 17.
FT DOMAIN 942 978 EGF-LIKE 18.
FT DOMAIN 980 1021 EGF-LIKE 19.
FT DOMAIN 1023 1205 LAMININ G-LIKE 1.
FT DOMAIN 1207 1243 EGF-LIKE 20.
FT DOMAIN 1250 1480 LAMININ G-LIKE 2.
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FT	DISULFID	571	580	BY SIMILARITY.	DT	10-OCT-2003 (Rel. 42, Last annotation update)
FT	DISULFID	586	597	BY SIMILARITY.	DE	Versican core protein precursor (large fibroblast proteoglycan)
FT	DISULFID	591	602	BY SIMILARITY.	DE	(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glia)
FT	DISULFID	604	610	BY SIMILARITY.	DE	hyaluronate-binding protein) (GHAP).
FT	DISULFID	613	624	BY SIMILARITY.	GN	CPSG2.
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FT	DISULFID	659	673	BY SIMILARITY.	OC	Bovidae; Bovinae; Bos.
FT	DISULFID	675	684	BY SIMILARITY.	OX	NCBI_TaxID=9913;
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FT	DISULFID	696	711	BY SIMILARITY.	RP	SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3).
FT	DISULFID	713	722	BY SIMILARITY.	RC	TISSUE=Forebrain;
FT	DISULFID	729	740	BY SIMILARITY.	RX	MEDLINE=98288320; PubMed=9624174;
FT	DISULFID	734	749	BY SIMILARITY.	RA	Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
FT	DISULFID	751	760	BY SIMILARITY.	RA	Zimmermann D.R.;
FT	DISULFID	767	778	BY SIMILARITY.	RT	"Versican V2 is a major extracellular matrix component of the mature
FT	DISULFID	772	787	BY SIMILARITY.	RT	bovine brain."
FT	DISULFID	789	799	BY SIMILARITY.	RL	J. Biol. Chem. 273:15758-15764(1998).
FT	DISULFID	806	817	BY SIMILARITY.	RP	[2]
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FT	DISULFID	849	890	BY SIMILARITY.	RX	MEDLINE=92062692; PubMed=1720020;
FT	DISULFID	892	901	BY SIMILARITY.	RT	Perides G., Biviano F., Signami A.;
FT	DISULFID	908	918	BY SIMILARITY.	RT	"Interaction of a brain extracellular matrix protein with hyaluronic
FT	DISULFID	930	939	BY SIMILARITY.	RT	acid."
FT	DISULFID	946	957	BY SIMILARITY.	RL	Biochim. Biophys. Acta 1075:248-258(1991).
FT	DISULFID	952	966	BY SIMILARITY.	CC	-!- FUNCTION: May play a role in intercellular signaling and in
FT	DISULFID	968	977	BY SIMILARITY.	CC	connecting cells with the extracellular matrix. May take part in
FT	DISULFID	984	995	BY SIMILARITY.	CC	the regulation of cell motility, growth and differentiation. Binds
FT	DISULFID	989	1009	BY SIMILARITY.	CC	hyaluronic acid.
FT	DISULFID	1011	1020	BY SIMILARITY.	CC	-!- SUBUNIT: Interacts with FBLN1 (by similarity).
FT	DISULFID	1211	1222	BY SIMILARITY.	CC	-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
FT	DISULFID	1216	1231	BY SIMILARITY.	CC	-!- ALTERNATIVE PRODUCTS:
FT	DISULFID	1233	1242	BY SIMILARITY.	CC	Event=Alternative splicing; Named isoforms=4;
FT	DISULFID	1485	1496	BY SIMILARITY.	CC	Comment=Additional isoforms seem to exist;
FT	DISULFID	1490	1505	BY SIMILARITY.	CC	Name=V0;
FT	DISULFID	1507	1516	BY SIMILARITY.	CC	ISOID=P81282-1; Sequence=Displayed;
FT	DISULFID	1573	1774	BY SIMILARITY.	CC	Name=V1;
FT	DISULFID	1768	1783	BY SIMILARITY.	CC	ISOID=P81282-2; Sequence=VSP_003078, VSP_003079;
FT	DISULFID	1785	1794	BY SIMILARITY.	CC	Name=V2;
FT	DISULFID	1801	1812	BY SIMILARITY.	CC	ISOID=P81282-3; Sequence=VSP_003080;
FT	DISULFID	1806	1821	BY SIMILARITY.	CC	Name=V3;
FT	DISULFID	1823	1832	BY SIMILARITY.	CC	ISOID=P81282-4; Sequence=VSP_003078, VSP_003081;
FT	DISULFID	1839	1850	BY SIMILARITY.	CC	TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed
FT	DISULFID	1844	1859	BY SIMILARITY.	CC	in the central nervous system, and in a number of mesenchymal and
FT	DISULFID	1861	1870	BY SIMILARITY.	CC	epithelial tissues; the major isoform V2 is restricted to the
FT	DISULFID	1878	1889	BY SIMILARITY.	CC	central nervous system.
FT	DISULFID	1883	1903	BY SIMILARITY.	CC	-!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
FT	DISULFID	1905	1914	BY SIMILARITY.	CC	(by similarity).
FT	DISULFID	1919	1930	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
FT	DISULFID	1924	1939	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 2 link domains.
FT	DISULFID	1924	1939	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 2 EGF-like domains.
FT	DISULFID	1941	1950	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 1 C-type lectin family domain.
FT	DISULFID	1957	1968	BY SIMILARITY.	CC	-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
FT	DISULFID	1962	1977	BY SIMILARITY.	CC	-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
Query Match					CC	-----
Best Local Similarity 100.0%; Score 34; DB 1; Length 2139;					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
QY 1 CTCVP 5					CC	the European Bioinformatics Institute. There are no restrictions on its
					CC	use by non-profit institutions as long as its content is in no way
Db 1903 CTCVP 1907					CC	modified and this statement is not removed. Usage by and for commercial
					CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
					CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
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RESULT 12					CC	EMBL; AF060456; AAC24358.1; -
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AC P81282; O77609; O77610; O77611; O77612;					DR	EMBL; AF060459; AAC24361.1; -
					DR	PIR; T14274; T14274.

DR PIR; T42389; T42389.  
 DR HSP; P01132; LEPC.  
 DR InterPro; IPR000152; Asx hydroxyl s.  
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 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR007110; Ig-like.  
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 DR InterPro; IPR001304; Lentin\_C.  
 DR InterPro; IPR000538; Link.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00008; EGF; 2.  
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 DR Pfam; PF00059; lectin\_c; 1.  
 DR Pfam; PF00084; sushi\_1.  
 DR Pfam; PF00193; Xlink; 2.  
 DR PRINTS; P01265; LINKMODULE.  
 DR ProDom; PD000918; Link; 2.  
 DR SMART; SM00032; CCF; 1.  
 DR SMART; SM00034; CLECT; 1.  
 DR SMART; SM00179; EGF CA; 1.  
 DR SMART; SM00409; IG\_1.  
 DR SMART; SM00445; LINK; 2.  
 DR PROSITE; PS00010; ASX HYDROXYL; 1.  
 DR PROSITE; PS00615; C-TYPE LECTIN\_1; 1.  
 DR PROSITE; PS00641; C-TYPE LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; 2.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 2.  
 DR PROSITE; PS01187; EGF CA; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR PROSITE; PS01241; LINK; 2.  
 DR GlycoProtein; Proteoglycan; Lentin; Extracellular matrix; Sushi;  
 KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;  
 KW Hyaluronic acid; Alternative splicing.  
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 Db 3098 CTCVP 3102  
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 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Versican core protein precursor (large fibroblast proteoglycan)  
 DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Gial  
 DE hyaluronate-binding protein) (GHAP).  
 GN CSFG2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM V0).  
 RX MEDLINE=95105186; PubMed=7528742;  
 RA Naso M.F., Zimmermann D.R., Iozzo R.V.;  
 RT "Characterization of the complete genomic structure of the human  
 RT versican gene and functional analysis of its promoter.";  
 RL J. Biol. Chem. 269:32999-33008(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM V1).  
 RC TISSUE=Placenta;  
 RX MEDLINE=90059882; PubMed=2583089;  
 RA Zimmermann D.R., Ruoslahti E.;  
 RT "Multiple domains of the large fibroblast proteoglycan, versican.";  
 RL EMBO J. 8:2975-2981(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM V2).  
 RC TISSUE=Glia; tumor;  
 RX MEDLINE=95105187; PubMed=7806529;  
 RA Dours-Zimmermann M.T., Zimmermann D.R.;  
 RT "A novel glycosaminoglycan attachment domain identified in two

alternative splice variants of human versican.";  
 J. Biol. Chem. 269:32992-32998(1994).  
 [4]  
 CC SEQUENCE OF 2711-3396 FROM N.A.  
 CC TISSUE=Lung fibroblast;  
 CC MEDLINE=88007514; PubMed=2820964;  
 CC Kruusius T., Gehlsen K.R., Ruoslahti E.;  
 CC "A fibroblast chondroitin sulfate proteoglycan core protein contains  
 CC lectin-like and growth factor-like sequences.";  
 CC J. Biol. Chem. 262:13120-13125(1987).  
 CC [5]  
 CC SEQUENCE OF 251-347 FROM N.A.  
 CC MEDLINE=93122792; PubMed=1478664;  
 CC Iozzo R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,  
 CC McPherson J.D.;  
 CC "Mapping of the versican proteoglycan gene (CSPG2) to the long arm of  
 CC human chromosome 5 (5q12-5q14).";  
 CC Genomics 14:845-851(1992).  
 CC [6]  
 CC SEQUENCE FROM N.A. (ISOFORM V3).  
 CC TISSUE=Brain;  
 CC MEDLINE=95181355; PubMed=7876137;  
 CC Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;  
 CC "Expression of PG-M(V3), an alternatively spliced form of PG-M  
 CC without a chondroitin sulfate attachment in region in mouse and human  
 CC tissues.";  
 CC J. Biol. Chem. 270:3914-3918(1995).  
 CC [7]  
 CC SEQUENCE OF 3333-3396 FROM N.A. (ISOFORM VINT).  
 CC TISSUE=Aortic smooth muscle;  
 CC MEDLINE=99327053; PubMed=10397680;  
 CC Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,  
 CC Wright T.N.;  
 CC "Versican/PG-M isoforms in vascular smooth muscle cells.";  
 CC Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).  
 CC [8]  
 CC PARTIAL SEQUENCE.  
 CC TISSUE=Brain;  
 CC MEDLINE=89174663; PubMed=2466833;  
 CC Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;  
 CC "Isolation and partial characterization of a glial  
 CC hyaluronate-binding protein.";  
 CC J. Biol. Chem. 264:5981-5987(1989).  
 CC [9]  
 CC TISSUE SPECIFICITY OF ISOFORMS.  
 CC MEDLINE=96213482; PubMed=8627343;  
 CC Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;  
 CC "Differential expression of versican isoforms in brain tumors.";  
 CC J. Neuropathol. Exp. Neurol. 55:528-533(1996).  
 CC -!- FUNCTION: May play a role in intercellular signaling and in  
 CC connecting cells with the extracellular matrix. May take part in  
 CC the regulation of cell motility, growth and differentiation. Binds  
 CC hyaluronic acid.  
 CC -!- SUBUNIT: Interacts with PBLN1 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=5;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=V0;  
 CC IsoId=P13611-1; Sequence=Displayed;  
 CC Name=V1;  
 CC IsoId=P13611-2; Sequence=VSP\_003082, VSP\_003083;  
 CC Name=V2;  
 CC IsoId=P13611-3; Sequence=VSP\_003084;  
 CC Name=V3;  
 CC IsoId=P13611-4; Sequence=VSP\_003082, VSP\_003085;  
 CC Name=Vint;  
 CC IsoId=P13611-5; Sequence=VSP\_003086;  
 CC -!- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed  
 CC in normal brain, gliomas, medulloblastomas, schwannomas,  
 CC neurofibromas, and meningiomas; V2 is restricted to normal brain  
 CC and gliomas; V3 is found in all these tissues except  
 CC medulloblastomas.

-----  
 -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development.  
 -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 -!- SIMILARITY: Contains 2 link domains.  
 -!- SIMILARITY: Contains 2 EGF-like domains.  
 -!- SIMILARITY: Contains 1 C-type lectin family domain.  
 -!- SIMILARITY: Contains 1 Sushi (SCR) domain.  
 -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.  
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 CC -----  
 CC EMBL; U16306; AAA65018.1; -.  
 CC EMBL; X15998; CAA34128.1; -.  
 CC EMBL; S52488; AAR24878.1; -.  
 CC EMBL; U26555; AAA67565.1; -.  
 CC EMBL; D32039; BAA06801.1; -.  
 CC EMBL; J02814; AAA36437.1; -.  
 CC EMBL; AF084545; AAD48545.1; -.  
 CC PIR; S06014; A60979.  
 CC HSP; P01132; IEGF.  
 CC Genew; HGNC:2464; CSPG2.  
 CC MIM; 118661; -.  
 CC GO; GO:0005578; C:extracellular matrix; TAS.  
 CC GO; GO:0005540; F:hyaluronic acid binding; TAS.  
 CC GO; GO:0008037; P:cell recognition; TAS.  
 CC GO; GO:0007275; P:development; TAS.  
 CC InterPro; IPR000152; Asx\_hydroxyl\_S.  
 CC InterPro; IPR000742; EGF\_2.  
 CC InterPro; IPR001881; EGF\_Ca.  
 CC InterPro; IPR006209; EGF\_Like.  
 CC InterPro; IPR007110; IG\_Like.  
 CC InterPro; IPR003599; Ig.  
 CC InterPro; IPR001304; Lectin\_C.  
 CC InterPro; IPR000538; Link\_CCP.  
 CC InterPro; IPR000436; Sushi\_SCR\_CCP.  
 CC Pfam; PF00008; EGF; 2.  
 CC Pfam; PF00084; sushi; 1.  
 CC Pfam; PF00193; Xlink; 2.  
 CC PRINTS; PR01265; LINKMODULE.  
 CC ProDom; PD000918; Link; 2.  
 CC SMART; SM00032; CCP; 1.  
 CC SMART; SM00034; CLECT; 1.  
 CC SMART; SM00179; EGF\_CA; 1.  
 CC SMART; SM00409; IG; 1.  
 CC SMART; SM00445; LINK; 2.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 CC PROSITE; PS00041; C\_TYPE\_LLECTIN\_2; 1.  
 CC PROSITE; PS00022; EGF\_1; 2.  
 CC PROSITE; PS01186; EGF\_2; 1.  
 CC PROSITE; PS00026; EGF\_3; 2.  
 CC PROSITE; PS01187; EGF\_CA; 1.  
 CC PROSITE; PS00835; IG\_Like; 1.  
 CC PROSITE; PS01241; LINK; 2.  
 CC Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;  
 CC Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;  
 CC Hyaluronic acid; Alternative splicing.  
 CC SIGNAL 1 20 POTENTIAL.  
 CC CHAIN 21 3396 VERSICAN CORE PROTEIN.  
 CC DOMAIN 21 146 IG-LIKE V-TYPE.  
 CC DOMAIN 167 244 LINK 1.  
 CC DOMAIN 265 346 LINK 2.  
 CC DOMAIN 348 1335 GAG-ALPHA  
 CC (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN).  
 CC DOMAIN 1336 3089 GAG-BETA.  
 CC DOMAIN 3089 3125 EGF-LIKE 1.  
 CC DOMAIN 3127 3163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
 CC

```
FT DOMAIN 3176 3290 C-TYPE LECTIN.
FT DOMAIN 3295 3353 SUSHI.
FT DISULFID 44 130 BY SIMILARITY.
FT DISULFID 172 243 BY SIMILARITY.
FT DISULFID 196 217 BY SIMILARITY.
FT DISULFID 270 345 BY SIMILARITY.
FT DISULFID 294 315 BY SIMILARITY.
FT DISULFID 3093 3104 BY SIMILARITY.
FT DISULFID 3098 3113 BY SIMILARITY.
FT DISULFID 3115 3124 BY SIMILARITY.
FT DISULFID 3131 3142 BY SIMILARITY.
FT DISULFID 3136 3151 BY SIMILARITY.
FT DISULFID 3153 3162 BY SIMILARITY.
FT DISULFID 3169 3180 BY SIMILARITY.
FT DISULFID 3197 3289 BY SIMILARITY.
FT DISULFID 3265 3281 BY SIMILARITY.
FT DISULFID 3296 3339 BY SIMILARITY.
FT DISULFID 3325 3352 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 100.0%; Score 34; DB 1; Length 3396;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 3113 CTCVP 3117

RESULT 14
VMSA HPBV0
ID VMSA HPBV0 STANDARD; PRT; 226 AA.
AC P31873;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297159; PubMed=2841200;
RA Rivkina M.B., Lunin V.G., Mahov A.M., Tikchenenko T.I., Kukain R.A.;
RT "Nucleotide sequence of integrated hepatitis B virus DNA and human
RT flanking regions in the genome of the PLC/PRP/5 cell line.";
RL Gene 64:285-296(1988).
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CC -----
DR EMBL; M21030; AAA45516.1; -
DR PIR; J04820; CAA28506.1; -.
DR F01; J04820; SAVLHV.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25476 MW; BFC4329CF1720600 CRC64;
Query Match 97.1%; Score 33; DB 1; Length 226;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 147 CTCIP 151

Search completed: April 8, 2004, 11:11:08
Job time : 4.16667 secs
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Qy 1 CTCVP 5
Db 147 CTCIP 151

RESULT 15
VMSA HPBV0
ID VMSA HPBV0 STANDARD; PRT; 226 AA.
AC P31868;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus (subtype ad).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31511;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89143494; PubMed=2465492;
RA Okamoto H., Omi S., Wang Y., Itoh Y., Tada F., Tanaka T., Akahane Y.,
RA Miyakawa Y., Mayumi M.;
RT "The loss of subtypic determinants in alleles, d/y or w/x, on
RT hepatitis B surface antigen.";
RL Mol. Immunol. 26:197-205(1989).
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CC -----
DR EMBL; M27765; AAA45518.1; -
DR PIR; PLO053; SAVLAD.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25348 MW; AFC12BCF3B08DC83 CRC64;
Query Match 97.1%; Score 33; DB 1; Length 226;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 147 CTCIP 151

Search completed: April 8, 2004, 11:11:08
Job time : 4.16667 secs
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